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GenCore version 5.1.3
 Copyright (C) 1993 - 2002 Compugen Ltd.
 1 Protein - Protein search, using sw model
 run on: October 11, 2002, 19:30:13 ; Search time 86 Seconds
 (without alignments)
 52.301 Million cell updates/sec
 title: US-09-794-764-195
 perfect score: 139
 sequence: 1 GKPNTNKEAERKSHDTQTQEICE 26
 scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 searched: 582222 seqs, 172994929 residues
 total number of hits satisfying chosen parameters: 5622222
 minimum DB seq length: 0
 maximum DB seq length: 2000000000
 post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries
 database : SPTREMBL19:*

Q9gyx7 mus musculus
 Q9lun7 arabidopsis
 O76734 dictyostelium
 O31611 bacillus subtilis
 Q9vwq6 drosophila
 Q9vwo3 drosophila
 Q9ryy9 mus musculus
 Q9bn1 plasmidium
 Q9bm12 plasmidium
 Q9bt7 homo sapien
 Q9po39 homo sapien
 Q96ab9 homo sapien
 Q93yz3 arabidopsis
 Q9zav0 mus musculus
 Q9owt3 mus sp. betta
 Q83072 treponema pallidum
 O96137 plasmidium
 O97294 plasmidium
 O15790 plasmidium
 O15799 plasmidium
 O9ng77 plasmidium
 O15788 plasmidium
 Q9ne4 arabidopsis
 O9sob7 arabidopsis
 Q9gvj7 mus musculus
 Q9pm16 campylobacter
 Q9srt4 arabidopsis
 Q9y563 homo sapien

DT 01-OCT-2000 (T-EMBLrel. 15, Created)
 DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (T-EMBLrel. 15, Last annotation update)

DE SEROREACTIVE ANTIGEN BMNI-17 (FRAGMENT).

OS Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.

CX NCBI_TAXID=5868;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MNL;

RX MEDLINE=20231818; PubMed=10768973;

RA Lodes M.J., Houghton R.L., Bruinsma E.S., Mohamath R., Reynolds L.D., Benson D.R., Krause P.J., Reed S.G., Persing D.H.;

RA "Serological expression cloning of novel immunoreactive antigens of Babesia microti.";

RT Infect. Immun. 68: 2783-2790 (2000).

RL DR AF206526; AAF68253.1; -.

PV NON_TMR 396 396

SEQUENCE 396 AA; 44720 MW; 706E153BA5EE6B7C CRC64;

Query Match 100.0%; Score 139; DB 5; Length 396;
 Best Local Similarity 100.0%; Pred. No. 6.8e-12; Indels 0; Gaps 0;
 Matches 26; Conservative 0; Mismatches 0; RT

Qy 1 GKPNTKSEKAERKSHDQTQEQICE 26
 Db 133 GKPNTKSEKAERKSHDQTQEQICE 158

RESULT 3

ID Q20227 PRELIMINARY; PRT; 879 AA.
 AC Q20227;
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)

DE F40F8_5. PROTEIN

GN F40F8_5.

OS Caenorhabditis elegans.

CC Metazoa; Nematoda; Chronadorea; Rhabditoidea;

CX Rhabditidae; Peloderainae; Caenorhabditis.

NCBI_TAXID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RA Macdougall R.;

RN Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.

[2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode *C. elegans*: A platform for investigating biology.";
 RL Science 202:2012-2018 (1998).
 DR EMBL; Z69302; CAA93361.1; -.

DR InterPro: IPR003439; ABC_TRANSPORTER; UNKNOWN_1;

DR PROST1; PS00211; ABC_TRANSPORTER; UNKNOWN_1;

SO SEQUENCE 879 AA; 97694 MW; BE4403D316B7E3C2 CRC64;

Query Match 43.5%; Score 60.5%; DB 5; Length 879;
 Best Local Similarity 52.2%; Pred. No. 2.4%; Indels 1; Gaps 1;
 Matches 12; Conservative 5; Mismatches 5; RT

Qy 5 TNKSEK-AERKSHDQTQEQICE 26
 Db 3 TNKREKQLEREHQEQTSQAVCE 25

RESULT 4

Q12037 PRELIMINARY; PRT; 1048 AA.

AC Q12037;

DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)

DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)

DE HYPOTHETICAL PROTEIN LI1309.

GN SCD25 OR SCD25 OR LI1309/SCD25 OR YLI016W.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycetes.

OC Saccharomyctaceae; Saccharomyces.

OC NCBI_TAXID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ALPHA S288C;

RA Purnelle B.; Goffeau A.;

RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.

[2]

RN [2]

RP SEQUENCE FROM N.A.

RA Goffeau A.; Purnelle B.;

RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

[3]

RN [3]

RP SEQUENCE FROM N.A.

RA Miosga T.; Zimmermann F.K.;

RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

[4]

RN [4]

RP SEQUENCE FROM N.A.

RA MIPS;

RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

[5]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=88405918; PubMed=8810043;

RA Miosga T.; Zimmermann F.K.;

RT "Sequence analysis of the CEN12 region of *Saccharomyces cerevisiae* on a 43.7 kb fragment of chromosome XII including an open reading frame homologous to the human cystic fibrosis transmembrane conductance regulator protein CFTR.";

RT Yeast 12:693-708 (1996).

RN [6]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=91094833; PubMed=1986720;

RA Damak F.; Boy-Narcotte E.; Le Roscouet D.; Guilbaud R.; Jacquet M.;

RT "CDC25, a CDC25-like gene which contains a RAS-activating domain and is a dispensable gene of *Saccharomyces cerevisiae*.";

RL Mol. Cell. Biol. 11:202-212 (1991).

RN [7]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=931087480; PubMed=1454190;

RA Rippmaster T.L.; Vaughn G.P.; Woolford J.L. Jr.;

RT "A putative ATP-dependent RNA helicase involved in *Saccharomyces cerevisiae* ribosome assembly.";

RL Proc. Natl. Acad. Sci. U.S.A. 89:11131-11135 (1992).

RN [8]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=94375516; PubMed=8089172;

RA Burgess S.M.; Delanoy M.; Jensen R.E.;

RT "MM1 encodes a mitochondrial outer membrane protein essential for establishing and maintaining the structure of yeast mitochondria.";

RT J. Cell. Biol. 126:1375-1391 (1994).

RN [9]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [10]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [11]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [12]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [13]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

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RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

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RL J. Cell. Biol. 130:553-566 (1995).

RN [14]

RP SEQUENCE FROM N.A.

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RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [15]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

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RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [16]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [17]

RP SEQUENCE FROM N.A.

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RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [18]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [19]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [20]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [21]

RP SEQUENCE FROM N.A.

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RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [22]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

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RL J. Cell. Biol. 130:553-566 (1995).

RN [23]

RP SEQUENCE FROM N.A.

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RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [24]

RP SEQUENCE FROM N.A.

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RL J. Cell. Biol. 130:553-566 (1995).

RN [25]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

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RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [26]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

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RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [27]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

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RL J. Cell. Biol. 130:553-566 (1995).

RN [28]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

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RL J. Cell. Biol. 130:553-566 (1995).

RN [29]

RP SEQUENCE FROM N.A.

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RL J. Cell. Biol. 130:553-566 (1995).

RN [30]

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RL J. Cell. Biol. 130:553-566 (1995).

RN [31]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

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RL J. Cell. Biol. 130:553-566 (1995).

RN [32]

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RL J. Cell. Biol. 130:553-566 (1995).

RN [33]

RP SEQUENCE FROM N.A.

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RL J. Cell. Biol. 130:553-566 (1995).

RN [34]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

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RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [35]

RP SEQUENCE FROM N.A.

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RL J. Cell. Biol. 130:553-566 (1995).

RN [36]

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RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [37]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

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RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

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RL J. Cell. Biol. 130:553-566 (1995).

RN [38]

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RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

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RL J. Cell. Biol. 130:553-566 (1995).

RN [39]

RP SEQUENCE FROM N.A.

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RL J. Cell. Biol. 130:553-566 (1995).

RN [40]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

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RL J. Cell. Biol. 130:553-566 (1995).

RN [41]

RP SEQUENCE FROM N.A.

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RL J. Cell. Biol. 130:553-566 (1995).

RN [42]

RP SEQUENCE FROM N.A.

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RL J. Cell. Biol. 130:553-566 (1995).

RN [43]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

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RL J. Cell. Biol. 130:553-566 (1995).

RN [44]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

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RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [45]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

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RL J. Cell. Biol. 130:553-566 (1995).

RN [46]

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RL J. Cell. Biol. 130:553-566 (1995).

RN [47]

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RL J. Cell. Biol. 130:553-566 (1995).

RN [48]

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RL J. Cell. Biol. 130:553-566 (1995).

RN [49]

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RL J. Cell. Biol. 130:553-566 (1995).

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RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

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RN [51]

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RN [52]

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RN [53]

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RL J. Cell. Biol. 130:553-566 (1995).

RN [54]

RP SEQUENCE FROM N.A.

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RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [55]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [56]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [57]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [58]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [59]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [60]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [61]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [62]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [63]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [64]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;

RA Gamble A.E.; Kurihara L.J.; Vallee R.B.; Rose M.D.;

RT "DNM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";

RL J. Cell. Biol. 130:553-566 (1995).

RN [65]

RP SEQUENCE FROM N.A.

RC STRAIN=FY-3 /RD005 (DERIVED FROM S288C);

RX MEDLINE=953348179; PubMed=7622557;</p

	DR	Pfam; PF00618; RasGEF; SMART; SM00147; RasGEF;	SEQUENCE FROM N.A.
	DR	PROSITE; PS00720; GDS_CD025; 1;	REDACTED
SO	SEQUENCE	1048 AA; 121960 MW; 40A1F12F9B86F458 CRC64;	REDACTED
	Query Match	Score 54; DB 3; Length 1048;	REDACTED
	Best Local Similarity	45.0%; Pred. No. 24;	REDACTED
	Matches	9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;	REDACTED
Qy	3	PNTNKESEKAERKSHDPTQTY 22	REDACTED
Db	1002	PNSNSNNKSGQEKSRRDDQTG 1021	REDACTED
<hr/>			
	RESULT 5		[2]
	ID Q9JG50	PRELIMINARY;	SEQUENCE FROM N.A.
	AC O9JG50;	PRT; 661 AA.	REDACTED
	DT 01-OCT-2000	(TREMBLrel. 15, Created)	REDACTED
	DT 01-OCT-2000	(TREMBLrel. 15, Last sequence update)	REDACTED
	DT 01-DEC-2001	(TREMBLrel. 19, Last annotation update)	REDACTED
	DE ORF1..		REDACTED
	OS TTV-like mini virus.		REDACTED
	Viruses; ssDNA viruses; Circoviridae.		REDACTED
	OC NCBI_TaxID=93678;		REDACTED
	RN [1]		REDACTED
	RP	SEQUENCE FROM N.A.	REDACTED
	RC	STRAIN=TLMV-NLC026;	REDACTED
	RA	Mishiro S., Hiiikata M., Takahashi K.;	REDACTED
	RL	Submitted (FEB-2000) to the EMBL/GenBank/DDJB databases.	REDACTED
	RN [2]		REDACTED
	RP	SEQUENCE FROM N.A.	REDACTED
	RC	STRAIN=TLMV-NLC026;	REDACTED
	RA	Takahashi K., Hiiikata M., Sanokhalov E.I., Mishiro S.;	REDACTED
	RT	"Full or near full length nucleotide sequences of TT virus variants (types SANBAN and YONBANYU) and the TT virus-like mini virus."	REDACTED
	RT	Intervirology 43:119-123,(2000).	REDACTED
	RL	EMBL: AB038630; BAA93609; 11; -.	REDACTED
	DR	InterPro; IPR04219; TT_CRF1.	REDACTED
	DR	Pfam; PF02956; TT_ORF1; 1.	REDACTED
	SQ	SEQUENCE 661 AA; 78995 MW; 83CE5F93A1AD286A CRC64;	REDACTED
	Query Match	Score 52.5%; DB 12; Length 661;	REDACTED
	Best Local Similarity	51.7%; Pred. No. 25;	REDACTED
	Matches	15; Conservative 3; Mismatches 6; Indels 5; Gaps 2;	REDACTED
Qy	3	11: : : : : : ERKSHDPTQTY-ICE 26	REDACTED
Db	566	PNTNKESEKA---ERKSHDPTQTY-ICE 26	REDACTED
<hr/>			
	RESULT 6		[2]
	Q9Z7W9	PRELIMINARY;	SEQUENCE FROM N.A.
	AC Q9Z7W9;	PRT; 651 AA.	REDACTED
	DT 01-MAY-1999	(TREMBLrel. 10, Created)	REDACTED
	DT 01-MAY-1999	(TREMBLrel. 10, Last sequence update)	REDACTED
	DT 01-DEC-2001	(TREMBLrel. 19, Last annotation update)	REDACTED
	DE SIMILARITY TO CHLPS INCA (CPJ0585 PROTEIN).		REDACTED
	GN CPN0585 OR CPJ0585 OR CP0163.		REDACTED
	OS Chlamydia pneumoniae (Chlamyphila pneumoniae).		REDACTED
	OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamyphila.		REDACTED
	OX NCBI_TaxID=83558;		REDACTED
	RN [1]		REDACTED
	RP	SEQUENCE FROM N.A.	REDACTED
	RC	STRAIN=CMW029;	REDACTED
	RA	Kalman S., Mitchell R., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grunwood J., Davis R.W., Stephens R.S.;	REDACTED
	RT	"Comparative genomes of Chlamydia pneumoniae and C. trachomatis." Nat. Genet. 21:385-389(1999).	REDACTED
<hr/>			

RX	MEDLINE=98135459; PubMed=9475118;
Qy	6 NKSEKAERKSHDTOTTOETOE 26
DR	: : PRELIMINARY; PRT; 3268 AA.
Qy	707 NKSFKPKNEKMDKRSLOEVYIE 727
DR	: : PRELIMINARY; PRT; 3268 AA.
RESULT 11	
ID Q03280	PRELIMINARY; PRT; 3268 AA.
AC Q03280; 01-NOV-1996 (TREMBLrel. 01, Created)	
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
DT D8035-1P (UBIQUITIN LIGASE).	
TM1 OR D8035-1 OR YDR457W.	
GN Saccharomyces cerevisiae (Baker's yeast).	
OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces; Saccharomyces; Saccharomycetaceae; Saccharomyces.	
OC NCBI_TaxID=49322;	
RN SEQUENCE FROM N.A.	
RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A., Hunicker-Smith S., Chen H., Cherry J.M., Chung E., Duncan M., Komp C., Hyman E., Kashkar D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X., Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N., Winant A., Yelton M., Botstein D., Davis R.W., Submitted (AUG-1995) to the EMBL/GenBank/DBJ;	
RL RN	SEQUENCE FROM N.A.
RA Dietrich F.S., Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.	
RL RN	SEQUENCE FROM N.A.
RA Utsugi T., Kikuchi Y., Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.	
RL RN	SEQUENCE OF 2156-3268 FRM N.A.
RA SMART; SMC00110; HECTC; 1.	
DR DR	Best Local Similarity 44.0%; Pred. No. 2.9e+02;
KW Ligase.	Matches 11; Conservative 6; Mismatches 6; Indels 2; Gaps 1;
SQ SEQUENCE 3268 AA; 374180 MW; 8F71F3493D70A6C9 CRC64;	
Pfan; PF00632; HECT.	
DR DR	Query Match 36.0%; Score 50; DB 3; Length 3268;
DR SMART; SMC00110; HECTC; 1.	Best Local Similarity 44.0%; Pred. No. 2.9e+02;
KW Ligase.	Matches 11; Conservative 6; Mismatches 6; Indels 2; Gaps 1;
RESULT 12	
ID Q92951	PRELIMINARY; PRT; 273 AA.
AC Q92951; 01-FEB-1997 (TREMBLrel. 02, Created)	
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)	
DT 01-FEB-2001 (TREMBLrel. 19, Last annotation update)	
ZINC FINGER PROTEIN.	
Homo sapiens (Human).	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
NCBI_TaxID=9606;	
OX Palmito M., Pittman G.S., Pan S., Pollard J., Purji V., Rees M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., SEQUENCE FROM N.A.	
RP	

Scoring table:	BLOSUM62	Description				
Gapped:	10.0	Gapext: 0.5				
Searched:	105224 seqs., 38719550 residues	Total number of hits satisfying chosen parameters: 105224				
Minimum DB seq length:	0					
Maximum DB seq length:	2000000000					
Post-processing:	Minimum Match: 0%					
	Maximum Match: 100%					
	Listing first: 45 summaries					
Database :	Swissprot_40 *					
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
		SUMMARIES				
Result No.	Score	Query				
Length	Match	DB ID				
		Description				
1	56	40	3	511	1	MDJ1_YEAST
2	54	38	8	1158	1	RL14_HUMAN
3	54	38	8	1253	1	SC25_YEAST
4	50	36	0	1409	1	AEX3_CAEEL
5	49	35	3	210	1	ON22_ARATH
6	47	33	8	120	1	TRI7_HUMAN
7	47	33	8	178	1	FXY5_HUMAN
8	47	33	8	369	1	VP6_AHSV3
9	47	33	8	369	1	VP6_AHSV6
10	47	33	8	2363	1	SPCO_MOUSE
11	46	33	8	533	1	YN34_YEAST
12	45	32	4	148	1	CALM_EUGGR
13	45	32	4	263	1	SGS3_DROYR
14	45	32	4	798	1	YCO0_MCPN
15	45	32	4	843	1	YMS1_YEAST
16	45	32	4	929	1	RBMA_HUMAN
17	45	32	4	1020	1	NPH_HUMAN
18	44	32	0	906	1	YK01_ARCFU
19	44	31	7	60	1	CENC_MOUSE
20	44	31	7	327	1	RL32_DETRA
21	44	31	7	328	1	HUNB_MANSE
22	44	31	7	343	1	SLAM_MOUSE
23	44	31	7	1903	1	YJL3_YEAST
24	43.5	31	3	178	1	YK01_ARCFU
25	43	30	9	52	1	RR32_CYACA
26	43	30	9	56	1	RL32_MCPN
27	43	30	9	63	1	RL32_XYLFA
28	43	30	9	325	1	LXBL_PHOLE
29	43	30	9	406	1	SNX6_HUMAN
30	43	30	9	406	1	YDLB_SFPHO
31	43	30	9	436	1	Y868_CHLMU
32	43	30	9	547	1	OM6C_CHLTR
33	43	30	9	547	1	OM6D_CHLTR

ALIGNMENTS

RESULT 1	
MDJ1_YEAST	
ID MDJ1_YEAST	
AC F35191;	
DT 01-FEB-1994 (Rel. 28, Created)	
DT 01-FEB-1994 (Rel. 28, Last sequence update)	
DT 16-OCT-2001 (Rel. 40, Last annotation update)	
DE MDJ1 protein mitochondrial precursor.	
GN MNJ1 OR YF016C.	
OS Saccharomyces cerevisiae (Baker's yeast).	
QC Eukaryota; Fungi; Ascomycota; Saccharomycetidae; Saccharomyces.	
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.	
OX NCBI_TAXID=4932;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=S288C / AB972;	
RA Bowley N.K., Prip-Buus C., Westermann B., Brown C.M., Schwartz E., Barrell B.G., Neupert W.; Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.	
RL [12]	
RN [12]	
RP SEQUENCE FROM N.A.	
RC STRAIN=S288C / AB972;	
RA Barrell B.G., Churcher C., Rutherford M.A.; Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.	
RN [3]	
SEQUENCE FROM N.A.	
RC STRAIN=S288C / AB972; PubMed=7670463;	
RX MEDLINE=95-0029; PubMed=7670463;	
RA Naitou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma S.-I., Sasamori M., Tsuchiya Y., Soeda E., Yokoyama K., Yamazaki M., Tashiro H., Eki T.; RT Analysis of the nucleotide sequence of chromosome VI from Saccharomyces cerevisiae.	
RL Nat. Genet. 10:261-268(1995).	
CC FOLDING	-1 - PLAYS A ROLE IN MITOCHONDRIAL BIOGENESIS AND PROTEIN SUBCELLULAR LOCATION: Mitochondrial.
CC -1 - SIMILARITY: CONTAINS 1 J CR DOMAIN.	
CC -1 - SIMILARITY: CONTAINS 1 CR DOMAIN.	
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.ebi.ac.uk/announce/ or send an email to license@ebi.ac.uk).	
CC DR EMBL; 228336; CAA82199.1; DR EMBL; 246255; CAA86351.1; DR EMBL; D50617; BAA09222.1; DR EMBL; D4456; BAA08011.1; DR SGD; S0001878; MDJ1.	

DR	InterPro; IPR003095; DnaJ.	
DR	InterPro; IPR002938; DnaJ-C.	
DR	InterPro; IPR001305; DnaJ.	
DR	InterPro; IPR001622; DnaJ-CXGXG.	
DR	Pfam; PF00226; DnaJ_N.	
DR	Pfam; PF01556; DnaJ_C; 1.	
DR	Pfam; PF00684; DnaJ_CXGXG; 1.	
DR	SMARTS; SM00271; DnaJ; 1.	
DR	PROSITE; PS00636; DnaJ_-; 1.	
DR	PROSITE; PS00637; DnaJ_CXXGXG; 1.	
DR	Chaperone; Heat shock; Mitochondrion; Repeat; Transit peptide.	
KW	MITOCHONDRIAL PROTEIN (POTENTIAL).	
FT	TRANSIT 1 55 J-DOMAIN.	
FT	CHAIN 56 511 MDD1 PROTEIN.	
FT	DOMAIN 59 127 GLY-RICH.	
FT	REPEAT 130 186 CXXGXG MOTIF.	
FT	REPEAT 230 237 CXXGXG MOTIF.	
FT	REPEAT 247 254 CXXGXG MOTIF.	
FT	REPEAT 269 276 CXXGXG MOTIF.	
FT	REPEAT 285 292 CXXGXG MOTIF.	
SQ	SEQUENCE 511 AA; 55561 MW; 007343427C66D2B6 CRC64;	
Query Match Score 40.3%; Best Local Similarity 50.0%; Matches 11; Conservative 2; Pred. No. 2; Mismatches 9; Indels 0; Gaps 0;	Score 56; DB 1; Length 511; Best Local Similarity 46.2%; Pred. No. 8.9; Matches 12; Conservative 3; Mismatches 11; Indels 0; Gaps 0;	Score 54; DB 1; Length 1158; Best Local Similarity 46.2%; Pred. No. 8.9; Matches 12; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
QY	3 PNTNNSERAERKSHDTQTEI 24	QY 1 GKPNTNKSEKAERKSHDTQTEICE 26
Db	90 PDNKEPDAEKKHDLQAYEI 111	Db 718 GNPNGKSEKETPLRDESTQEHSE 743
RESULT 2	SC25_YEAST	RESULT 3
RI14_HUMAN	STANDARD	ID SC25_YEAST
AC P48552	PRT; 1158 AA.	AC P14771
DT 01-FEB-1996 (Rel. 33, Created)		DT 01-APR-1990 (Rel. 14, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)		DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)		DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Nuclear factor RIP140 (Nuclear receptor interacting protein 1).		DE SCD25 protein.
GN NRP1.		GN SCD25 OR SDC25
OS Homo sapiens (Human).		OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		OC Eukaryota; Fungi; Ascomycotina; Saccharomycetes.
MMU Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		OC Saccharomyctales; Saccharomyctaceae; Saccharomyces.
NCBI_TaxID=9606;		NCBI_TaxID=4932;
RN [1]		RN [1]
RP SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.
RC ISSUE-PERIOD		RC STRAIN=W303;
RX MEDLINE=95369446; PubMed=761693;		RX MEDLINE=91094833; PubMed=1986220;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park H.-S., Toyota A., Ishii K., Totoki Y., Choi D.-K., Ohki M., Takagi T., Rump A., Schillihabel M., Taudien S., Blechschmidt K., Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D., Reichwald K., Rosenthal A., Kudoh J., Schuhd A., Zimmerman W., Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E., Minoshima S., Shimizu N., Nordwick G., Hornischer K., Brandt P., Schober M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H., Ransier J., Beck A., Klages S., Hennig S., Riessmann L., Dagand E., Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F., Lehrich H., Reinhard R., Yaspo M.-L.;	RA Boy-Marcotte E., Damak F., Camonis J., Garreau H., Jacquinet M.; RA "The C-terminal part of a gene partially homologous to CDC 25 gene suppresses the cdc25-5 mutation in Saccharomyces cerevisiae.";	
RT "Nuclear factor RIP140 modulates transcriptional activation by the estrogen receptor."		RT "Enhancement of the GDP-GTP exchange of RAS proteins by the carboxy-terminal domain of SCD25.";
RT EMBJ J. 14:3741-3751(1995).		RT Science 248:866-868(1990).
RN [2]		RN [4]
RP SEQUENCE FROM N.A.		RP FUNCTION
RC MEDLINE=20289799; PubMed=10830953;		RC MEDLINE=90260533; PubMed=2188363;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park H.-S., Toyota A., Ishii K., Totoki Y., Choi D.-K., Ohki M., Takagi T., Rump A., Schillihabel M., Taudien S., Blechschmidt K., Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D., Reichwald K., Rosenthal A., Kudoh J., Schuhd A., Zimmerman W., Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E., Minoshima S., Shimizu N., Nordwick G., Hornischer K., Brandt P., Schober M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H., Ransier J., Beck A., Klages S., Hennig S., Riessmann L., Dagand E., Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F., Lehrich H., Reinhard R., Yaspo M.-L.;	RA Boy-Marcotte E., Damak F., Poulet P., Mistou M.-Y., Parneggiani A., Camonis J., Creciet J.B., Jacquinet M.; RA "Enhancement of the GDP-GTP exchange of RAS proteins by the carboxy-terminal domain of SCD25.";	
RT The DNA sequence of human chromosome 21."		RT RP FUNCTION
RL Nature 405:311-319(2000).		RL MEDLINE=91156112; PubMed=2000228;
CC RECEPTOR: MODULATES TRANSCRIPTIONAL ACTIVATION BY THE ESTROGEN RECEPTOR.		CC MEDLINE=91156112; PubMed=2000228;
CC		CC Boy-Marcotte F., Baril R., Camonis J., Boy-Marcotte E.,

RT RT The COOH-domain of the product of the *Saccharomyces cerevisiae* SCD25 gene elicits activation of p21-ras proteins in mammalian cells.;

RL RN OncoGene 6:347-349(1991).

CC -!- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP.

CC -!- MISCELLANEOUS: SUPPRESSES THE CDC25-5 MUTATION IN YEAST (RESTORES CAMP LEVEL) AND HAS SIMILAR FUNCTIONS AS CDC25.

CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

CC -!- SIMILARITY: CONTAINS 1 RASEF DOMAIN.

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CC DR EMBL; M26647; AAA16365.1; -.

CC DR InterPro: IPR001895; RasGDP_CDC25.

CC DR InterPro: IPR001452; SH3_Pfam; PF00177; S14177.

CC DR PIR: S14177; S14177.

CC DR DR EMBL; M26647; AAA16365.1; -.

CC DR PROSTE; PS00020; GDS_CD25; 1.

CC DR PROSTE; PS50002; SH3; 1.

CC DR SMART; SM00229; RasGEF; 1.

CC DR SMART; SM00326; SH3; 1.

CC DR SMART; SM00147; RasGEF; 1.

CC DR SMART; SM00229; RasGEF; 1.

CC DR PROSTE; PS00020; GDS_CD25; 1.

CC DR PROSTE; PS50002; SH3; 1.

KW Guanine-nucleotide releasing factor; Cell cycle; Cell division; SH3 domain.

FT DOMAIN 26 98 SH3.

FT DOMAIN 74 79 POLY-ASN.

FT DOMAIN 434 437 POLY-ARG.

FT VARIANT 584 590 DVVVKPI -> V (IN STRAIN QL136).

SEQUENCE 1253 AA; 144379 MW; 2DDE2C9EC27E5E60D CRC64;

Query Match Best Local Similarity 45.0%; Pred. No. 9.6%; Length 1253; Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0; RESULT 5 OM22_ARATH

ID OM22_ARATH STANDARD; PRT; 210 AA.

AC B82873; Q9PZJ6; STANDARD; PRT; 210 AA.

AC B82873; Q9PZJ6; STANDARD; PRT; 210 AA.

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Mitochondrial import receptor subunit TOM20-2 (Translocase of outer membrane 20 kDa Subunit 2).

GN TOM20-2 OR ATIG2/390 OR F17L21.18.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophytina; Embryophytina.

OC Spermatophytina; Magnoliophytina; eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TAXID:3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV_COLUMBIA;

RC PubMed=11130712;

RA Werhahn W.; Niemeyer A.; Jaensch L.; Krift V.; Schmitz U.K., BRAUN H.-P.;

RT Purification and characterization of the preprotein translocae of the outer mitochondrial membrane from *Arabidopsis thaliana*.

RT Identification of multiple forms of TOM20.;"

RL Plant Physiol. 125:943-954 (2001).

RN SEQUENCE FROM N.A.

RC STRAIN=CV_COLUMBIA;

RC PubMed=21016719; PubMed=11130712;

RA Theologis A.; Ecker J.R.; Palm C.J.; Fedderspiel N.A.; Kaul S., White O.; Alonso J.; Altaba H.; Araujo R.; Bowman C.L.; Brooks S.Y., Leimbach E.; Chan A.; Chao Q.; Chen H.; Cheuk R.F.; Chin C.W., RA Buehler E.

TISSUE-Bone marrow;
EX MEDLINE-2124016; PubMed#11342114;
OMSA T , Chen Y.G. , Mantalaris A , Wu J.H.D.;
"A cDNA from human bone marrow encoding a protein exhibiting homology
to the ATP11/PLM/MAT8 family of transmembrane proteins."
Biochim Biophys Acta 1517:307-310(2001).
-|- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-|- SIMILARITY: BELONGS TO THE FXYD FAMILY.

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EMBL; R	AF161452;	AAF29077;	1;	-;		
EMBL; R	BC009642;	AHH09642;	1;	-;		
EMBL; R	AF177940;	AAG09301;	1;	-;		
InterPro; R	IPR000272;	ATP1G1_PLM_MAT8.				
Pfam; R	PF02036;	ATP1G1_PLM_MAT8;	1.			
PROSITE; R	PS01310;	FXYD;	1.			
		Transmembrane;	Signal;	Ionic channel;		
		Alternative splicing;	Polymorphism.			
SIGNAL	1	21		POTENTIAL		
CHAIN	22	178		FXYD DOMAIN-CONTAINING ION TRANSPORT		
DOMAIN	22	145		REGULATOR 5.		
TRANSMEM	1.46	164		EXTRACELLULAR (POTENTIAL).		
DOMAIN	165	178		POTENTIAL.		
VARSPLIC		97		CYTOSPLASMIC (POTENTIAL).		
				MSPSGCLLITVGLLPRQHQLKDTTSSSSADSTIMDQ		
				VPTRAPDAVYTELQTSPTWPAQQTQLEQNDI		
				GPIWMDPHEPKSTKA -> MOTIV-ENTPCGT-HGSCT-PSPTD-		
				GPIWMDPHEPKSTKA -> MOTIV-ENTPCGT-HGSCT-PSPTD-		

RESULT 8					
P6_AHSV3	VP6_AHSV3	STANDARD;	PRT;	369 AA.	
O	O61909;				
T	Q61909;				
T	15-DEC-1998 (Rel. 37, Created)				
T	15-DEC-1998 (Rel. 37, Last sequence update)				
T	15-DEC-1998 (Rel. 37, Last annotation update)				
V	VP6 protein (Minor inner core protein VP6).				
S9.	African horse sickness virus 3 (AHSV-3) (African horse sickness virus (serotype 3))				
S	dsRNA viruses; Reoviridae; Orbivirus				
S	Virus types:				

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RESULT 9						
VP6_AHSV6		STANDARD;		PRT; 369 AA.		
ID	VP6_AHSV6	AC	Q64913;	Created		
Query Match	33.8%	Score	47;	DB	1;	Length 369;
Best Local Similarity	52.9%	Pred.	No.	25;		
Matches 9;	Conservative	2;	Mismatches	6;	Indels	0;
Matches					caps	0;
QY	6 NKSEKAERKSHDTQATQ 22					
	: :					
Db	49 NKSEKEENKTHDDRRVE 65					
RESULT 10						
VP6_AHSV6						
ID	VP6_AHSV6	AC	Q64913;	Created		
DT	15-DEC-1998	(Rel.	37,	Last sequence update)		
DT	15-DEC-1998	(Rel.	37,	Last annotation update)		
DT	15-DEC-1998	(Rel.	37,			
DE	VP6 protein	(Minor inner core protein VP6).				
GN	S9.	African horse sickness virus 6 (AHSV-6) (African horse sickness virus (serotype 6)).				
OS		Virususes: dsRNA viruses: Reoviridae: Orbivirus.				
OC						

OX NCBI_TAXID=86066;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96335674; PubMed=8757982;
RA Turnbull P.J.; Cormack S.; Huismans H.;
RT "Characterization of the gene encoding core protein VP6 of two
RT African horse sickness virus serotypes.";
RT J. Gen. Virol. 77:1421-1423 (1996).
RL -|- SIMILARITY: BELONGS TO THE REOVIRUSES VP6 FAMILY.

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CC ----- CC
DR U33000; AAB17107_1;
DR IPR01399; Orbi_VP6.
DR PF01516; Orbi_VP6_1.
KW Core protein.
SQ SEQUENCE 369 AA; 38450 MW; 1ECCCOFFFF21FFF9 CRC64;
Query Match 33.8%; Score 47; DB 1; Length 369;
Best Local Similarity 52.9%; Pred. No. 25;
Matches 9; Conservative 2; Mismatches 6; Indels 0; caps 0;
QY 6 NKSEKAERKSHDFTORTO 22
QY ||||| | | || : -
```

RESULT_10	SPCO_MOUSE	STANDARD;	PRT;	2363 AA.
ID	SPCO_MOUSE			
AC	062267			
DT	01-NOV-1997	(Rel. 35, Created)		
DT	01-NOV-1997	(Rel. 35, Last sequence update)		
DT	01-MAR-2002	(Rel. 41, Last annotation update)		

DE Spectrin beta chain, brain 1 (Spectrin, non-erythroid beta chain 1)
 DE (Beta-II spectrin) (Fodrin beta chain).
 GN SPTBN1 OR SPTB2 OR SPNB2 OR SPNB2.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

NCBI_TAXID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/C;

RX MEDLINE=93240985; PubMed=8479293;

RX Ma Y., Zimmer W.E., Riederer B.M., Goodman S.R.;

RX "The complete amino acid sequence for brain beta spectrin (beta fodrin): relation to globin sequences.";

RX Brain Res. Mol. Brain Res. 18:87-89(1993).

RN [2]

RP STRUCTURE BY NMR OF 2199-2304.

RX MEDLINE=94268558; PubMed=9208297;

RX Macias M.J., Musacchio A., Ponstingl H., Nilges M., Saraste M.,

RX Oschkinat H.;

RX "Structure of the pleckstrin homology domain from beta-spectrin";

RX Nature 369:675-677(1994).

RN [3]

RP STRUCTURE BY NMR OF 2199-2304.

RX MEDLINE=97342712; PubMed=199409;

RX Macias M.J., Musacchio A., Ponstingl H., Nilges M., Oschkinat H.;

RX "Automated NOESY interpretation with ambiguous distance restraints:

RX the refined NMR solution structure of the pleckstrin homology domain

RX from beta-spectrin.";

RX J. Mol. Biol. 269:408-422(1997).

RN [4]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 2199-2304.

RX MEDLINE=96030773; PubMed=5885597;

RX Hyvonen M., Macias M.J., Nilges M., Oschkinat H., Saraste M.,

RX Wilmanas M.;

RX "Structure of the binding site for inositol phosphates in a PH

RX domain.";

RX EMBO J. 14:4676-4681(1995).

CC -1- FUNCTION: FODRIN, WHICH SEEKS TO BE INVOLVED IN SECRETION,

CC INTERACTS WITH CALMODULIN IN A CALCIUM-DEPENDENT MANNER AND IS
 CC THUS CANDIDATE FOR THE CALCIUM-DEPENDENT MOVEMENT OF THE
 CC CYTOSKELETON AT THE MEMBRANE.

CC -1- SUBUNIT: LIKE ERTHROCYTE SPECTRIN, THE SPECTRIN-LIKE PROTEINS
 CC ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO
 CC TETRAMERS.

CC -1- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.

CC -1- SIMILARITY: CONTAINS 2 CALPONIN HOMOLOGY (CH) DOMAINS.

CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.

CC -1- SIMILARITY: CONTAINS 17 SPECTRIN REPEATS.

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CC EMBL; M74773; AAC42040.1; -.

DR PDB; 1BTN; 08-MAR-96.

DR MGD; MGI: 983388; Spnb2.

DR InterPro; IPR001589; Actinin_act_bind.

DR InterPro; IPR001715; Calponin_hom.

DR InterPro; IPR001849; PH.

DR InterPro; IPR002017; Spectrin.

DR Pfam; PF00307; CH; 2.

DR Pfam; PF00169; PH; 1.

DR PRINTS; PF00435; spectrin; 18.

DR SMART; SM00033; CH; 1.

DR SMART; SM00233; PH; 1.

DR EMBL; U23084; AAC49105.1; -.

DR SMART; SM001150; SPEC; 16.				
DR PROSITE; PS00019; ACTININ_1;				
DR PROSITE; PS00020; ACTININ_2;				
DR PROSITE; PS50022; CH; 2.				
DR PROSITE; PS50003; PH_DOMAIN; 1;				
KW Cytoskeleton; Membrane; Repeat; Actin-binding; Capping protein; 3D-structure.				
FT DOMAIN	1	275	ACTIN-BINDING (BY SIMILARITY).	
FT DOMAIN	54	158	CH 1.	
FT DOMAIN	173	275	CH 2.	
FT REPEAT	276	384	SPECTRIN 1.	
FT REPEAT	385	498	SPECTRIN 2.	
FT REPEAT	499	608	SPECTRIN 3.	
FT REPEAT	609	714	SPECTRIN 4.	
FT REPEAT	715	819	SPECTRIN 5.	
FT REPEAT	820	925	SPECTRIN 6.	
FT REPEAT	926	1032	SPECTRIN 7.	
FT REPEAT	1033	1139	SPECTRIN 8.	
FT REPEAT	1140	1245	SPECTRIN 9.	
FT REPEAT	1246	1350	SPECTRIN 10.	
FT REPEAT	1351	1462	SPECTRIN 11.	
FT REPEAT	1463	1562	SPECTRIN 12.	
FT REPEAT	1563	1668	SPECTRIN 13.	
FT REPEAT	1669	1775	SPECTRIN 14.	
FT REPEAT	1776	1881	SPECTRIN 15.	
FT REPEAT	1882	1987	SPECTRIN 16.	
FT REPEAT	1988	2132	SPECTRIN 17.	
FT DOMAIN	2196	2306	PH.	
SEQUENCE	2363 AA;	274420 MW;	64C9E4BD26BBC7B8 CRC64;	
Query Match	33.8%	Score 47;	DB 1;	Length 2363;
Matches 9;	Best Local Similarity 37.5%;	Pred. No. 1.7e-02;		
	Conservative 5;	Mismatches 10;	Indices 0;	Gaps 0;
Qy 3 PNTNKSEKAERKSHDTQTTOBICE 26				
Db 2105 PNTKVSEAEASQWDTSKGDQVSO 2128				

RESULT 11

YN34_YEAST

ID YN34_YEAST

STANDARD;

PRT;

533 AA.

AC P48565;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 05-MAY-2000 (Rel. 39, Last annotation update)

DE Hypothetical 61.5 kDa protein in CLA4-P154 intergenic region.

GN YNL294C OR N0466.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryote; Fungi; Ascomycota; Saccharomycotina; Saccharomyces.

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OC NCBI_TAXID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RA Maurer K.C.T.; Urbanus J.H.M.; Planta R.J.;

RA RT *Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV

RA RT carried by a ribosomal protein gene cluster, the genes encoding a

RA RT plasma membrane protein and a subunit of replication factor C, and a

RA RT novel putative serine/threonine protein kinase gene.;"

RL Yeast 11:1303-1310(1995).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC --

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CC --

CC DR PROSITE; PS28C / FY1679;

CC DR MEDLINE=S26132033; PubMed=8553702;

CC DR RA Maurer K.C.T.; Urbanus J.H.M.; Planta R.J.;

CC RT *Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV

CC RT carried by a ribosomal protein gene cluster, the genes encoding a

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CC --

CC DR EMBL; U23084; AAC49105.1; -.

DR	EMBL; Z71570; CAA96212.1;	-;						
KW	Hypothetical protein; Transmembrane.							
FT	TRANSMEM	95	115	POTENTIAL.				
FT	TRANSMEM	128	148	POTENTIAL.				
FT	TRANSMEM	179	199	POTENTIAL.				
FT	TRANSMEM	210	230	POTENTIAL.				
FT	TRANSMEM	248	268	POTENTIAL.				
FT	TRANSMEM	281	301	POTENTIAL.				
SQ	SEQUENCE	533 AA;	61532 MW;	9494A18512F399CC CRC64;				
Query Match	Best Local Similarity 33.1%; Matches 7;	Score 46; DB 1;	Length 533;					
Qy	7 KSEKAERKSHDQTQEQICE;	26						
Db	376 ESQDASTDRDTSSNEVCD	395						
RESULT 12	CALM_EUGGR	STANDARD;	PRT;	148 AA.				
AC	P11118;							
DT	01-JUL-1989 (Rel. 11, Created)							
DT	01-JUL-1989 (Rel. 11, Last sequence update)							
DT	30-MAY-2000 (Rel. 39, Last annotation update)							
DE	Calmodulin.							
OS	Euglenida gracilis.							
OC	Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.							
OX	NCBI_TaxID=3039;							
RN	[1]							
RP	SEQUENCE.							
RC	STRAIN=Z;							
RX	Medline=92241300; PubMed=1572365;							
RA	Toda H., Yazawa M., Yagi Y.;							
RT	"Amino acid sequence of calmodulin from Euglena gracilis.";							
RL	Eur. J. Biochem. 205:1653-1660(1992).							
CC	-1- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF ENZYMES BY CA(++) . AMONG THE ENZYMES TO BE STIMULATED BY THE CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND PHOSPHATASES.							
CC	-1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING SITES.							
CC	-1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.							
DR	PIR: JK0008; MCIG.							
DR	PIR; S21212; S21212.							
DR	HSSP; P02593; ICDM.							
DR	InterPro: IPR002048; EF-hand.							
DR	PFAM: PF00036; ehand; 4.							
DR	SMART: SM00054; EFh; 4.							
DR	PROSITE: PS00018; EF HAND; 4.							
KW	Calcium-binding; Repeat; Acetylation; Methylation.							
FT	MOD_RES	1	1	ACETYLATION.				
FT	MOD_RES	115	115	METHYLATION.				
FT	MOD_RES	148	148	METHYLATION.				
FT	CA_BIND	20	31	EF-HAND 1.				
FT	CA_BIND	56	67	EF-HAND 2.				
FT	CA_BIND	93	104	EF-HAND 3.				
FT	CA_BIND	129	140	EF-HAND 4.				
SQ	SEQUENCE	148 AA;	167244 MW;	82A1E48108638455 CRC64;				
Query Match	Best Local Similarity 64.3%; Matches 9;	Score 45; DB 1;	Length 148;					
Qy	13 RKSHDQTQEQICE	26						
Db	74 RKMHDPTEEKE	87						
RESULT 13	SGS3_DROYA	STANDARD;	PRT;	263 AA.				
ID	SGS3_DROYA	STANDARD;	PRT;	263 AA.				
AC	P13728;							
DT	01-JAN-1990 (Rel. 13, Created)							
DT	01-AUG-1991 (Rel. 19, Last sequence update)							
DT	16-Oct-2001 (Rel. 40, Last annotation update)							
DE	Salivary glue protein Sgs-3 precursor.							
GN	SGS3.							
OS	Drosophila yakuba (Fruit fly).							
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Aphidoidea; Drosophilidae; Drosophila.							
OC	NCBI_TaxID=7245;							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RX	Medline=88132966; PubMed=1138416;							
RA	Martin C.H., Mayeda C.A., Meyerowitz E.M.;							
RT	"Evolution and expression of the Sgs-3 glue gene of Drosophila."							
RL	J. Mol. Biol. 201:273-287(1988).							
CC	-1- DEVELOPMENTAL STAGE: PRODUCED BY THIRD-INSTAR LARVAE.							
DR	PfIR; S0136; S01360.							
DR	FLYBase; Flygn0013172; Dyak; Sgs3.							
KW	Repeat; Signal.							
FT	SIGNAL	1	23					
FT	CHAIN	24	263	Salivary Glue Protein SGS-3.				
SQ	SEQUENCE	263 AA;	28392 MW;	C0C3246BA82A261C CRC64;				
Query Match	Best Local Similarity 32.4%; Matches 8;	Score 45; DB 1;	Length 263;					
Qy	4 NTNKSSEKAERKSHDQTQEQICE	23						
Db	168 HTTKSPTSKRTHETTTSK 187							
RESULT 14	YC00_MYCPN	STANDARD;	PRT;	798 AA.				
ID	YC00_MYCPN	STANDARD;	PRT;	798 AA.				
AC	P50288;							
DT	16-OCT-2001 (Rel. 40, Created)							
DT	16-OCT-2001 (Rel. 40, Last sequence update)							
DT	16-OCT-2001 (Rel. 40, Last annotation update)							
DE	Hypothetical lipoprotein MPN200 precursor (Gr9_orf798).							
GN	MPN200 OR MP631.							
OS	Mycoplasma pneumoniae.							
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes; Mycoplasmataceae; Mycoplasma.							
OC	NCBI_TaxID=2104;							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RC	Strain=ATCC 29342 / M129;							
RX	Medline=96177562; PubMed=3604303;							
RA	Hilbert H., Himmelreich R., Plagens H., Herrmann R.;							
RT	"Sequence analysis of 56 kb from the genome of the bacterium Mycoplasma pneumoniae comprising the dnaA region, the atp operon and a cluster of ribosomal protein genes."							
RT	Nucleic Acids Res. 24:628-639(1996).							
RL	Nucleic Acids Res. 24:628-639(1996).							
RN	[12]							
RP	SEQUENCE FROM N.A.							
RC	Strain=ATCC 29342 / M129;							
RX	Medline=97105885; PubMed=8948633;							
RA	Hilbert H., Himmelreich R., Hilbert H., Plagens H., Pirkle E., Li B.-C., Herrmann R.;							
RT	"Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae."							
RT	Nucleic Acids Res. 24:4420-4449(1996).							
CC	-1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor (Potential).							
CC	-1- SIMILARITY: BELONGS TO THE MG185 / MG260 FAMILY.							
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CC	RESULTS							

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GenCore version 5.1.3

W protein - protein search: using SW model

join search, using sw model

run on : October 11, 2002, 20:28:08 ; Search time 48 Seconds
(without alignments)
52,048 Million cell update

5-09-794-764-195

Sequence: GKPNTNKSEKAÉRKSHDTQTQEICE 2

String table: BUSSM82 Gabor 10.0 Gapext 0.5

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Total number of hits satisfying chosen Parameters: 283138

minimum DB seq length: 0

maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first AE summaries

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PIR_1;*:1;*:21;*:21

2. pir2:*

P1R3:^{*} P1R4:^{*}
3: A:

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

result	No.	Score	Query Length	Match Length	ID	Description
	1	60.5	43.5	879	2	T22033 hypothetical prote
	2	56	40.3	511	2	S3898 heat shock protein
	3	54	38.8	1048	2	S6458 SCD25 protein (ver
	4	54	38.8	1280	2	S14177 SCD25 protein (ver
	5	51	36.7	651	2	F86663 hypothetical prote
	6	51	36.7	651	2	A72660 hypothetical prote
	7	50	36.0	196	2	T2245 glutamyl synthase
	8	50	36.0	465	2	JC5184 hypothetical prote
	9	50	36.0	471	2	AD2345 conserved hypoth
	10	50	36.0	579	2	D72092 hypothetical
	11	50	36.0	579	2	C86332 probable oxidoredu
	12	50	36.0	923	2	G81253 presynaptic activi
	13	50	36.0	1409	2	T37188 hypothetical prote
	14	50	36.0	3288	2	S69225 hypothetical prote
	15	49	35.3	803	2	T40036 hypothetical prote
	16	47.5	34.2	211	1	E6944 GTP Pyrophosphin
	17	47	33.8	453	2	probable hemolysin
	18	47	33.8	537	2	probable RNA helic
	19	47	33.8	635	2	hypothetical prote
	20	47	33.8	950	2	hypothetical prote
	21	47	33.8	1097	2	T45622 hypothetical prote
	22	46.5	33.5	65	2	GB1292 hypothetical prote
	23	46.5	33.5	1076	2	F98831 hypothetical prote
	24	46	33.1	557	2	T10457 L-protein L - Ps
	25	46	33.1	225	2	hypothetical prote
	26	46	33.1	283	2	hypothetical prote
	27	46	33.1	383	2	H90266 conserved hypoth
	28	46	33.1	533	2	S63370 probable membrane
	29	46	33.1	608	2	T22572 hypothetical prot

30	46	33.1	761	2	B679797
31	46	33.1	788	2	C95046
32	46	33.1	831	2	D479758
33	45.5	32.7	631	2	T13115
34	45.5	32.7	881	2	T334243
35	45.5	32.7	890	2	T344243
36	45.5	32.7	1230	2	T19899
37	45	32.4	148	1	MCEG
38	45	32.4	263	2	S01560
39	45	32.4	310	2	T47695
40	45	32.4	333	2	T19313
41	45	32.4	542	2	A46364
42	45	32.4	542	2	T02024
43	45	32.4	749	2	A45294
44	45	32.4	761	2	S66711
45	45	32.4	798	2	S62291

ALIGNMENT S

RESULT 1
T22033

RESULT 1
T22033
hypothetical protein F40F8.5 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*

submitted to the EMBL Data Library, February 1996
 A; Reference number: 219505
 A; Accession: T22033
 Status: preliminary; translated from GB/EMBL/DDJB
 A; Molecule type: DNA
 A; Residues: 1-879 <NWHL>
 A; Cross-references: EMBL:Z89302; PIDN:CAA93261.1; GSPDB:GN00020; CESP:F40F8.
 A; Experimental source: clone F40F8
 C; Genetics:
 A; Gene: CESP:F40F8.5
 A; Map position: 2
 A; Intron: 63/1; 149/1; 173/1; 217/1; 262/1; 306/1; 347/1; 381/2; 422/2; 440
 Query Match 43.5%; Score 60.5; DB 2; Length 879;
 Best Local Similarity 52.2%; Pred. No. 1.4;
 Matches 12; Conservative 5; Mismatches 5; Indels 1; Gaps 5
 QY 5 TNKSEK-AERKSHDQTQICE 26
 DB 3 TNFREKQIHFRECHQIKOSAVCE 25

RESULT 2

S38898 heat shock protein MDJ1 precursor - yeast (*Saccharomyces cerevisiae*)
 S38898 N;Alternate names: MDJ1 protein; protein YFL016c
 S38898 C;Species: *Saccharomyces cerevisiae*
 S38898 C;Date: 31-Dec-1993 #sequence_revision 27-Jan-1995 #text_change 20-J
 S38898 C;Accession: S38898; S48320; A5500; S56238; S62297
 S38898 C;Cross-references: EMBL:228336; NID:9431909; PIDN:CAA82189.1; PID:91
 S38898 R;Rowley, N. K.; Pip-Blaus, C.; Westermann, B.; Brown, C. M.; Schwarz, C.
 S38898 submitted to the EMBL Data Library, November 1993
 S38898 A;Description: Mdj1p, a novel DnaJ homologue of Saccharomyces cerevi
 S38898 A;Reference number: S38898
 S38898 A;Accession: S38898

S38898 A;Molecule type: DNA
 S38898 A;Residues: 1-511 <RDN>
 S38898 A;Cross-references: EMBL:246255; NID:9559925; PIDN:CAA86351.1; PID:g
 S38898 R;Churcher, C.
 S38898 Submitted to the EMBL Data Library, September 1994
 S38898 A;Accession number: S48310
 S38898 A;Molecule type: DNA
 S38898 A;Residues: 1-511 <CHU>
 S38898 A;Cross-references: EMBL:246255; NID:9559925; PIDN:CAA86351.1; PID:g
 S38898 R;Rowley, N. P.; Pip-Blaus, C.; Westermann, B.; Brown, C. M.; Schwarz, C.
 S38898 A;Accession: S48320

Cell 77, 249-259, 1994
A;Title: Mdj1p, a novel chaperone of the DnaJ family, is involved in mitochondrial biogenesis
A;Reference number: A53500; MUID:94221642
A;Accession: A53500
A;Molecule type: DNA
A;Residues: 1-511 <R02>
A;Cross-references: GB:Z28336; NID:9431909; PIDN:CAA82189_1; PID:9431910
R;Murakami, Y.; Naitou, M.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanuma submitted to the EMBL Data Library, May 1995
A;Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces cerevisiae
A;Accession: S56186
A;Molecule type: DNA
A;Residues: 1-511 <MUR>
A;Cross-references: EMBL:D50617; NID:9836685; PIDN:BAA09222_1; PID:9836738; MIPS:YFL016C
R;Murakami, Y.
submitted to the EMBL Data Library, December 1994
A;Reference number: S62230
A;Accession: S62297
A;Molecule type: DNA
A;Residues: 1-511 <MTW>
A;Cross-references: EMBL:D44596; NID:91100783; PIDN:BAA08001_1; PID:91100788
A;Gene: SGD:MDJ1
A;Cross-references: SGD:S0001878; MIPS:YFL016C
A;Map position: 6L
A;Genome: nuclear
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C;Keywords: heat shock; membrane protein; mitochondrial inner membrane; mitochondrion; mitochondrial peptide (mitochondrion) #status predicted <TPN>
F;I-55/Domain: transit peptide (mitochondrion) #status Predicted <MAT>
F;61-125/Domain: dnaJ amino-terminal homology <DNJ>
Query Match 40.3%; Score 56; DB 2; Length 511;
Best Local Similarity 50.0%; Pred. No. 3.6;
Matches 11; Conservative 2; Mismatches 9; Indels 0; Gaps 0;
Db 90 PNTNPKSEKAERKSHDQTQTEI 24
Db 90 PDINKPKDAEKFFHDLNQAYEI 111

RESULT 3
S64758
SCD25 protein (version 2) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein L1309; protein YLL016w
C;Species: Saccharomyces cerevisiae
C;Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 21-Jul-2000
R;Miosga, T.; Zimmermann, F.K.
submitted to the Protein Sequence Database, May 1996
A;Accession: S64758
A;Molecule type: DNA
A;Residues: 1-1048 <M10>
A;Cross-references: EMBL:273121; NID:91360186; PID:e245452; PID:91360187; MIPS:YLL016w
A;Experimental source: strain S288C
A;Reference number: S64761
A;Molecule type: DNA
A;Residues: 1-1048 <SOF>
A;Cross-references: EMBL:273121; NID:91360186; PID:e245452; PID:91360187; MIPS:YLL016w
R;Purnelle, B.; Goffeau, A.
A;Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals 14% similarity and a new ABC transporter homologous to the human multidrug resistance protein.
A;Accession: S63390
A;Molecule type: DNA
A;Residues: 1-1048 <PUR>

A;Cross-references: EMBL:X97560; NID:91297003; PID:e2388680; PID:91297014
R;Miosga, T.; Zimmermann, F.K.
Yeast 12, 693-708, 1996
A;Title: Sequence analysis of the CEN12 region of *Saccharomyces cerevisiae* on a 43.7 kb conductance regulator protein CfTR
A;Reference number: S70557; MUID:96405918
A;Accession: S70559
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1048 <NIW>
A;Cross-references: EMBL:X91488; NID:91495203; PIDN:CAAG62775_1; PID:91495207
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1999
C;Genetics:
A;Gene: SGD:SCD25; SDC25
A;Cross-references: SGD:S0003939; MIPS:YLL016w
A;Map position: 12L
C;Superfamily: CDC25-type guanine nucleotide exchange activator homology <SO3>
F;744-995/Domain: CDC25-type guanine nucleotide exchange activator homology <SO3>
Query Match 38.8%; Score 54; DB 2; Length 1048;
Best Local Similarity 45.0%; Pred. No. 14;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
Qy 3 PNTNPKSEKAERKSHDQTQTEI 22
Db 1002 PNSNSNNKSQEKSRRDDQTDE 1021

RESULT 4
S14177
SCD25 protein (version 1) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein L1309; protein YLL016w
C;Species: Saccharomyces cerevisiae
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 06-Feb-1998
C;Accession: S14177; PS0040
R;Damak, F.; Boy Marcotte, E.; Le-Roscouet, D.; Guilbaud, R.; Jacquet, M.
submitted to the EMBL Data Library, August 1989
A;Reference number: S14177
A;Accession: S14177
A;Molecule type: DNA
A;Residues: 1-1250 <DAM1>
A;Cross-references: EMBL:M26647
R;Damak, F.; Boy Marcotte, E.; Le-Roscouet, D.; Guilbaud, R.; Jacquet, M.
Mol. Cell. Biol. 11, 202-212, 1991
A;Title: SCD25, a CDC25-1-like gene, which contains a RAS-activating domain and is a di-A;Reference number: S12942; MUID:91094833
A;Accession: S12942
A;Molecule type: DNA
A;Residues: 1-737; 'A', '738-970', 'I', '972-1250 <DAM2>
A;Cross-references: EMBL:M26647
R;Damak, F.; Boy Marcotte, E.; Le-Roscouet, D.; Guilbaud, R.; Jacquet, M.
A;Note: the authors translated the codon GAG for residue 538 as Asp, GTC for residue 777 as Glu, and TGT for residue 972 as Cys.
R;Boy Marcotte, E.; Damak, F.; Camonis, J.; Garreau, H.; Jacquet, M.
Gene 77, 21-30, 1989
A;Title: The C-terminal part of a gene partially homologous to CDC25 gene suppresses a heat-shock response.
A;Accession: PS0040
A;Molecule type: DNA
A;Residues: 668-679, NPWMILMC', 689, 'N', 691-1250 <BOY>
A;Note: the authors translated the codon GCA for residue 747 as Asp and GAT for residue 748 as Asn.
C;Genetics:
A;Gene: SGD:SCD25; SDC25
A;Cross-references: SGD:S0003939; MIPS:YLL016w
A;Map position: 12L
C;Superfamily: CDC25-type guanine nucleotide exchange activator homology <SO3>
F;946-11197/Domain: CDC25-type guanine nucleotide exchange activator homology <SO3>
Query Match 38.8%; Score 54; DB 2; Length 1250;
Best Local Similarity 45.0%; Pred. No. 17;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
Qy 3 PNTNPKSEKAERKSHDQTQTEI 22
Db 1204 PNSNSNNKSQEKSRRDDQTDE 1223

RESULT 5

F86563 hypothetical protein CPJ0585 [imported] - Chlamydophila pneumoniae (strain J138)
 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
 Nucleic Acids Res. 28, 2311-2314, 2000
 A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A;Reference number: A86491; MUID:20330349
 A;Accession: F86563
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-651 <RBA>
 A;Cross-references: GB:BA000008; PIDN:98978957; PIDN:BA98792.1; GSPDB:GN00142
 A;Gene: CPJ0585

Query Match 36.7%; Score 51; DB 2; Length 651;
 Best Local Similarity 38.1%; Pred. No. 24;
 Matches 8; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 6 NKSEKAERKSHDTQTQEQICE 26
 Db 270 NQSQDIQRADREASQRACE 290

RESULT 6

A72060 hypothetical protein CP0163 [imported] - Chlamydophila pneumoniae (strains CWL029 and AF
 N;Alternate names: hypothetical Protein CPn0585
 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
 C;Accession: A/2060-881607
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
 R:Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
 Nature Genet. 21, 385-389, 1999
 A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
 A;Reference number: A72060; MUID:992066606
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-651 <RBA>
 A;Cross-references: GB:AE001643; GB:AE001363; NID:94376876; PIDN:AAD18724.1; PIDN:94376878
 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.; Nucleic Acids Res. 28, 1397-1406, 2000
 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A;Reference number: A81500; MUID:20150235
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-651 <RBA>
 A;Cross-references: GB:AE002117; GB:AE002161; NID:97189090; PIDN:AAF38042.1; PIDN:9718909

Query Match 36.7%; Score 51; DB 2; Length 651;
 Best Local Similarity 38.1%; Pred. No. 24;
 Matches 7; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 6 NKSEKAERKSHDTQTQEQICE 26
 Db 270 NQSQDIQRADREASQRACE 290

RESULT 7

T25445 hypothetical protein B0261.5 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: T25445
 R;Scheet, P.; Gattung, S.
 A;Description: The EMBL Data Library, April 1997 submitted to the EMBL Data Library, April 1997
 A;Reference number: Z20036
 A;Accession: T25445
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-196 <SCH>
 A;Cross-references: EMBL:U97016; PIDN:AAB52352.1; GSPDB:GN00019; CESP:B0261.5
 A;Experimental source: strain Bristol N2; clone B0261
 C;Genetics:
 A;Gene: CESP:B0261.5
 A;Map position: 1
 A;Introns: 162/3

Query Match 36.0%; Score 50; DB 2; Length 196;
 Best Local Similarity 43.5%; Pred. No. 9.9;
 Matches 5; Mismatches 8; Indels 0; Gaps 0;

Qy 2 KPNTNIKSEKAERKSHDTQTQEQI 24
 Db 105 KASDKKKANKKSPTQEQEV 127

RESULT 8

JC5184 glutamate synthase (GOGAT) (EC 1.4.1.-) small chain - Thiobacillus ferrooxidans
 C;Species: Thiobacillus ferrooxidans
 C;Accession: JC5184
 R;Deane, S.M.; Rawlings, D.E.
 Gene 177, 261-263, 1996
 A;Title: Cloning and sequencing of the gene for the Thiobacillus ferrooxidans ATCC330
 A;Reference number: JC5184; MUID:97080532
 A;Accession: JC5184
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-65 <DEA>
 A;Cross-references: GB:U36427; NID:91033069; PIDN:AAA79783.1; PIDN:g1033071
 A;Experimental source: strain ATCC33020
 C;Genetics:
 A;Gene: g1tD
 C;Superfamily: glutamate synthase small chain
 C;Keywords: iron-sulfur protein; metalloprotein; oxidoreductase
 F;151-156,291-296/Region: glycine-rich
 F;427-437/Region: FAD-binding #status predicted
 F;45,48,53,57,92,96,102,106/Binding site: iron-sulfur clusters (Cys) (covalent) #stat

Query Match 36.0%; Score 50; DB 2; Length 465;
 Best Local Similarity 50.0%; Pred. No. 23;
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 6 NKSEKAERKSHDTQTQEQIC 25
 Db 73 NRLEEPATLSHQNTPEIC 92

RESULT 9

AD2545 hypothetical protein alr7647 [imported] - Anabaena sp. (strain PCC 7120) plasmid pcc7
 C;Species: Anabaena sp.
 A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
 C;Accession: AD2545
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriku Nakazaki, N.; Shimpo, M.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
 A;Reference number: AB1807; MUID:21595285; PMID:11759840
 A;Accession: AD2545
 A;Status: preliminary

A: Molecule type: DNA
A: Residues: 1-471 <KUR>
A: Cross-references: PIDN:BA077290.1; PID:917134732; GSPDB:GN00181
A: Experimental source: strain FCC 7120
C: Genetics;
A: Gene: a7647
A: Genome: plasmid

Query Match 36.0%; Score 50; DB 2; Length 471;
Best Local Similarity 45.5%; Pred. No. 24;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Oy 3 PNTNKEAKRKSHTDTQEQI 24
Db 151 PNRNSTRAVNSKHTPTSKI 172

RESULT 10
D72092
Conserved hypothetical protein CP0426 [imported] - Chlamydophila pneumoniae (strains Cwl
N; Alternative names: ct082 hypothetical protein
C: Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C: Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C: Accession: D72092; B81577
B: Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A: Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A: Reference number: A72000; MUID:99206606
A: Accession: D72092
A: Status: Preliminary
A: Molecule type: DNA
A: Cross-references: GB:AE001617; GB:AE001363; NID:94376599; PID:9437660
A: Experimental source: strain Cwl029
B: Read, T.D.; Brunham, R.C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwynn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A: Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A: Reference number: A81500; MUID:20150255
A: Accession: B81577
A: Status: Preliminary
A: Molecule type: DNA
A: Cross-references: 1-579 <RA>
A: Experimental source: strain AR39, HL cells
C: Genetics: CP0426

Query Match 36.0%; Score 50; DB 2; Length 579;
Best Local Similarity 30.8%; Pred. No. 29;
Matches 8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Oy 1 GKPNTNKEAKRKSHTDTQEQICE 26
Db 287 GIPNSNTLERAKEAKQESSEQLSE 312

RESULT 11
C86532
CT082 hypothetical protein [imported] - Chlamydophila pneumoniae (strain J138)
C: Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C: Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C: Accession: C86532
B: Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is Nucleic Acids Res. 28, 2311-2314, 2000
A: Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A: Reference number: A86491; MUID:20330349
A: Accession: C86532
A: Status: Preliminary
A: Molecule type: DNA
A: Cross-references: 1-579 <STO>
A: Experimental source: strain J138

RESULT 14
S69625

C: Genetics;
A: Gene: CPJ0331
Query Match 36.0%; Score 50; DB 2; Length 579;
Best Local Similarity 30.8%; Pred. No. 29;
Matches 8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GKPNTNKEAKRKSHTDTQEQICE 26
Db 287 GIPNSNTLERAKEAKQESSEQLSE 312

RESULT 12
G81253
Probable oxidoreductase C11585C [Imported] - Campylobacter jejuni (strain NCTC 11168)
C: Species: Campylobacter jejuni
C: Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C: Accession: G81253
B: Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chil C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Ba Nature; 403, 665-668, 2000
A: Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A: Reference number: A81250; MUID:20150912
A: Accession: G81253
A: Status: Preliminary
A: Molecule type: DNA
A: Cross-references: GB:AU139079; GB:AU111168; NID:969668971; PIDN:CA873573.1; PID:96966
A: Experimental source: serotype O2, strain NCTC 11168
C: Genetics;
A: Gene: C11585C

RESULT 13
T31188
presynaptic activity regulator aex-3 - Caenorhabditis elegans
C: Species: Caenorhabditis elegans
C: Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000
C: Accession: T31188
B: Leimbac, D.; Minx, M.
Submitted to the EMBL Data Library, February 1996
A: Description: The sequence of C. elegans cosmid C02H7.
A: Reference number: 220523
A: Accession: T31188
A: Status: translated from GB/EMBL/DDJB
A: Molecule type: DNA
A: Residues: 1-1409 <LEI>
A: Cross-references: EMBL:U49945; PIDN: AAC47926.1; GSPDB:GN00029
A: Experimental source: strain Bristol N2; clone C02H7
C: Genetics:
A: Gene: aex-3; CESP:C02H7.3
A: Map Position: X
A: Introns: 77/1; 136/2; 183/2; 232/3; 283/3; 386/3; 427/3; 527/3; 577/1; 699/3; 782/2

Query Match 36.0%; Score 50; DB 2; Length 1409;
Best Local Similarity 32.0%; Pred. No. 71;
Matches 8; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 2 KPNTNKEAKRKSHTDTQEQICE 26
Db 769 QPNPTSQTANQSKNQTYKEFCD 793

hypothetical protein YDR457w - yeast (Saccharomyces cerevisiae)
 C;Species: Saccharomyces cerevisiae
 C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 23-Mar-2001

C;Accession: S69625

R;Dietrich, F.S.

submitted to the EMBL Data Library, August 1995

A;Description: The sequence of S. cerevisiae cosmids 9410, 8035, 8166, and 9787.

A;Reference number: S69554

A;Accession: S69625

A;Molecule type: DNA

A;Residues: 1-3268 >DIE>

A;Cross-references: EMBL:U33050; NID:g927726; PIDN:AAE64910.1; PID:g927738; MIPS:YDR457w

C;Genetics:

A;Gene: SGD:TOM1

A;Cross-references: SGD:S0002865; MIPS:YDR457w

A;Map position: 4R

Query Match	Score 36.0%	DB 2;	Length 3268;
Best Local Similarity	Pred. No. 1.6e-22;		
Matches 11;	Mismatches 6;	Indels 2;	Gaps 1;
Conservative			
QY 2 KPNTNKEAERKSHDTQTQEICE 26			
Db 226 KNNNETQTSIKV-TMTTQELCE 248			

RESULT 15

T40036 hypothetical protein SPBC27B12.12c - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C;Accession: T40036

R;Wood, V.; Rajandream, M.A.;

Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A.

submitted to the EMBL Data Library, December 1997

A;Reference number: Z21900

A;Accession: T40036

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-803 <WOO>

A;Cross-references: EMBL:AL021766; PIDN:CAA16907.1; GSPDB:GN00067; SPDB:SPBC27B12.12c

A;Experimental source: strain 972h; cosmid C27B12

C;Genetics:

A;Gene: SPBC27B12.12c

A;Map position: 2

Query Match	Score 35.3%	DB 2;	Length 803;
Best Local Similarity	Pred. No. 34.8%;		
Matches 8;	Mismatches 5;	Indels 0;	Gaps 0;
Conservative			
QY 2 KPNTNKEAERKSHDTQTQEI 24			
Db 150 KPQSNKKHRQRVVKHSPKSTLEV 172			

Search completed: October 11, 2002, 20:41:05
 Job time : 51 secs

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OM protein - protein search, using sw model

Run on: October 11, 2002, 18:23:07 ; Search time 62 Seconds

(without alignments)
 46,579 Million cell updates/sec

Title: US-09-794-764-195

Perfect score: 139
 Sequence: 1 GRPNTNKSEKAERKSHDTQTTQICE 26Scoring table: BLOSUM62
 Gapext 0.5

Searched: 74754 seqs, 11013796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Genesed_033802:*

1: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1980 DAT: *
 2: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1981.DAT: *
 3: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1982.DAT: *
 4: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1983.DAT: *
 5: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1984.DAT: *
 6: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1985.DAT: *
 7: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1986.DAT: *
 8: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1987.DAT: *
 9: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1988.DAT: *
 10: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1989.DAT: *
 11: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1990.DAT: *
 12: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1991.DAT: *
 13: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1992.DAT: *
 14: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1993.DAT: *
 15: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1994.DAT: *
 16: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1995.DAT: *
 17: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1996.DAT: *
 18: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1997.DAT: *
 19: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1998.DAT: *
 20: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA1999.DAT: *
 21: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA2000.DAT: *
 22: /SIDS1/gcddata/geneseq/geneseqp-emb1/AA2001.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	139	100.0	275	Babesia microti BM
2	139	100.0	275	Babesia microti an
3	139	100.0	275	B. microti clone
4	139	100.0	445	Babesia microti BM
5	139	100.0	445	Babesia microti an
6	139	100.0	445	B. microti BMN1-17
7	139	100.0	666	B. microti MN-10/B
8	139	100.0	1132	B. microti MN-10/B
9	63	45.3	32	AY24559
10	63	45.3	32	AAB30308
11	54	38.8	600	AAG75992

OS EP834567-A2.

XX PD 08-APR-1998.

XX PF 01-OCT-1997;

XX PR 24-APR-1997;

XX PR 01-OCT-1996;

XX PR 24-APR-1997;

PT infection and in protective vaccines
 XX Claim 1; Page 101-102; 113pp; English.
 PS
 XX The sequence is that of a polypeptide comprising at least
 CC one antigenic portion of a Babesia microti antigen. It can be used
 CC to diagnose B. microti infection by detecting specific antibodies
 CC in usual immunoassays. Infection can also be diagnosed using:
 CC (a) primers or probes derived from the coding sequence, in
 CC standard amplification or hybridisation tests, or (b) using
 CC antibodies to detect the corresponding antigen. It is also
 CC useful in vaccines to protect against infection, especially
 CC when formulated with an adjuvant. The new diagnostic methods
 CC allow rapid differentiation between B. microti infection and
 CC other tick-borne diseases (Lyme disease and ehrlichiosis) that
 CC have similar symptoms but require different treatments.
 XX Sequence 275 AA;
 SQ Query Match 100.0%; Score 139; DB 20; Length 275;
 Best Local Similarity 100.0%; Pred. No. 3.4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 YY 1 GKPNTNKEAERKSHDTQTQICE 26
 Db 218 GKPNTNKEAERKSHDTQTQICE 243
 RESULT 3
 AAB30217
 ID AAB30217 standard; Protein: 275 AA.
 XX
 AC AAB30217;
 XX 12-FEB-2001 (first entry)
 DT
 XX B. microti clone antigen SEQ ID NO: 53.
 DE B. microti clone antigen SEQ ID NO: 53.
 XX KW Babesiosis; rodent parasite; tick-borne illness; antigen;
 KW disease diagnosis; disease prevention.
 XX OS Babesia microti.
 XX PN WO200060090-A1.
 XX PD 12-OCT-2000.
 XX 05-APR-2000; 2000WO-US09136.
 PF XX 05-APR-2000; 2000WO-US09136.
 PR 05-APR-1999; 99US-0286488.
 PR 17-MAR-2000; 2000US-0528784.
 PA (CORTI -) CORIXA CORP.
 PA Reed SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD;
 XX PI Reed SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD;
 XX DR 2000-686939/67.
 XX New polypeptides containing an antigenic portion of Babesia microti
 PT antigen and DNAs encoding the polypeptides, useful for diagnosing,
 PT treating or preventing B. microti infection, or for inducing protective
 PT immunity in a patient.
 XX WPI; 2000-686939/67.
 XX Example 1; Page 98; 118pp; English.
 PS
 XX The present invention is related to the isolation of antigenic sequences
 CC from the rodent parasite Babesia microti. This organism is transmitted to
 CC humans by the same tick which transmits Lyme disease and ehrlichiosis.
 CC The organism causes a malaria-like infection known as babesiosis. The
 CC sequences identified by this invention can be used in the diagnosis,
 CC prevention and treatment of babesiosis.
 XX Sequence 275 AA;
 SQ Query Match 100.0%; Score 139; DB 21; Length 275;
 Best Local Similarity 100.0%; Pred. No. 3.4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 YY 1 GKPNTNKEAERKSHDTQTQICE 26
 Db 218 GKPNTNKEAERKSHDTQTQICE 243
 RESULT 4
 AAWS6298
 ID AAWS6298 standard; Protein: 445 AA.
 XX
 AC AAWS6298;
 XX DT 28-SEP-1998 (first entry)
 XX Sequence 275 AA;

The present invention describes isolated polypeptides comprising specific immunogenic portions of Babesia microti AAX88983 to AAX88994 and specifically claimed B. microti immunogenic proteins, and AAY24338 to AAY24339 represent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B. microti infections. The present sequence represents a B. microti antigen.

E	X	Babesia microti BMNI-17 complement antigen sequence.
X	X	antigen; detection; diagnosis; vaccine; tick-borne disease differentiation; Lyme disease; ehrlichiosis.
X	S	Babesia microti.
X	X	EPB34567-A2.
N	X	08-APR-1998.
X	D	01-OCT-1997: 97EP-01117067.
X	X	24-APR-1997; 97US-0845558.
R	R	01-OCT-1996; 96US-0723142.
X	X	(CORI-) CORIXA CORP.
A	X	Houghton R, Lodes MJ, Reed SG, Sleath PR;
I	X	WPI: 1998-195465/18.
R	X	N-PSDB; AAV22153.
X	X	Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid vectors, transformed cells and antibodies, useful for diagnosis infection, and protective vaccines.

X X The sequence is that of a polypeptide comprising at least
X X one antigenic portion of a Babesia microti antigen. It can
X X to diagnose B. microti infection by detecting specific anti-
X X bodies in the patient's serum. Infection can also be diagnosed using
X X in usual immunoassays. Infected patients can be diagnosed using
X X (a) primers or probes derived from the coding sequence, in
X X standard amplification or hybridisation tests, or (b) using
X X antibodies to detect the corresponding antigen. It is also
X X useful in vaccines to protect against infection, especially
X X when formulated with an adjuvant. The new diagnostic method
X X allows rapid differentiation between B. microti infection and other
X X tick-borne diseases (Lyme disease and ehrlichiosis) which
X X have similar symptoms but require different treatments.

Q	Sequence	445 AA;			
	Query Match	100.0%	Score 139;	DB 19;	Length 445;
	Best Local Similarity	100.0%	Pred. No. 5	9e-13;	
	Matches 26;	conservative	0;	Mismatches 0;	Indels 0;
Y					Gaps
					1 GKPTNKSEKAERKSHDPIQTTQEQICE 26

RESULT 5
 AAY24358
 D AAY24358 standard; protein; 445 AA.
 X
 C
 C
 AAY24358;
 X
 T 16-SEP-1999 (first entry)
 Babesia microti antigen BMNT-17 complementary open reading frame protein.
 E
 W Babesia microti; antigen; immunogen; diagnosis; infection; vaccine;
 X immunity; detection.
 W

S Babesia microti.
X WO929869-A1.
X 17-JUN-1999.
X

Query Match	Score	DB	Length	445;
Best Local Similarity	100.0%	Pred. No.	5,9e-13	
Matches	100.0%	Mismatches	0;	
Matches	26;	Conservative	0;	Gaps
QY	1	GKPNTNKSEKAERKSHDTOTQICE	26	0;
Db	182	GKPNTNKSEKAERKSHDTOTQICE	207	"
RESULT 6				
AAB30207				
ID				
ID AAB30207 standard; Protein; 445 AA.				
XX				
AC				
AAB30207;				
XX				
DT				
12-FEB-2001 (first entry)				
XX				
DE				
B. microti BMNI-17 antigen reverse complement SEQ ID NO: 38.				
XX				
DE				
Babesiosis; rodent parasite; tick-borne illness; antigen;				
XX				
KW				
Babesia diagnosis; disease prevention.				
XX				
OS				
Babesia microti.				
XX				
XX				
PN				
WO20060090-A1.				
XX				
PD				
12-OCT-2000.				
XX				
PF				
05-APR-2000; 2000WO-US09136.				
XX				
PR				
'05-APR-1999; 9905-0284488.				
XX				
PR				
17-MAR-2000; 2000US-0528784.				
XX				
PA				
(CORIXA) CORIXA CORP.				
XX				
PI				
Reed SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD,				
XX				
DR				
WPI: 2000-686939/67.				
XX				
PT				
New polypeptides containing an antigenic portion of Babesia microti				
PT				
antigen and DNAs encoding the polypeptides, useful for diagnosing,				
PT				
treating or preventing B. microti infection, or for inducing protective				
PT				
immunity in a patient.				
XX				
PS				
Example 1; Page 86-87; 118pp; English.				
XX				

CC The present invention is related to the isolation of antigenic sequences
 CC from the rodent parasite Babesia microti. This organism is transmitted to
 CC humans by the same tick which transmits Lyme disease and ehrlichiosis.
 CC The organism causes a malaria-like infection known as babesiosis. The
 CC sequences identified by this invention can be used in the diagnosis,
 CC prevention and treatment of babesiosis.

XX Sequence 445 AA;

Query Match 100.0%; Score 139; DB 21; Length 445;
 Best Local Similarity 100.0%; Pred. No. 5.9e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX

Qy 1 GKPNTNKEKERAERKSHTDTQEQICE 26

Db 182 GKPNTNKEKERAERKSHTDTQEQICE 207

RESULT 8
 AAB30231 standard; Protein; 1132 AA.
 ID AAB30231
 XX
 AC AAB30231:
 XX
 DT 12-FEB-2001 (first entry)

XX DE B. microti MN-10/BMNI-17 fusion protein SEQ ID NO: 87.
 XX KW Babesiosis; rodent parasite; tick-borne illness; antigen;
 XX KW disease diagnosis; disease prevention.
 XX OS Babesia sp.
 XX Synthetic.
 XX PN WO200060090-A1.
 XX PD 12-OCT-2000.
 XX PF 05-APR-2000; 2000WO-US09136.
 XX PR 05-APR-1999; 99US-0286488.
 XX PR 17-MAR-2000; 2000US-0528784.
 XX PA (CORTI-) CORIXA CORP.
 XX PI Reed SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD;
 XX WPI: 2000-686939/67.

XX DR 2000-686939/67.

XX PT New polypeptides containing an antigenic portion of Babesia microti

XX PT antigen and DNAs encoding the polypeptides, useful for diagnosing,

XX PT treating or preventing B. microti infection, or for inducing protective

XX PT immunity in a patient.

XX PS Example 7; Page 112-116; 118pp; English.

XX XX The present invention is related to the isolation of antigenic sequences

CC from the rodent parasite Babesia microti. This organism is transmitted to

CC humans by the same tick which transmits Lyme disease and ehrlichiosis.

CC The organism causes a malaria-like infection known as babesiosis. The

CC sequences identified by this invention can be used in the diagnosis,

CC prevention and treatment of babesiosis.

XX SQ Sequence 1132 AA;

XX DR 2000-686939/67.

XX PT New polypeptides containing an antigenic portion of Babesia microti

XX PT antigen and DNAs encoding the polypeptides, useful for diagnosing,

XX PT treating or preventing B. microti infection, or for inducing protective

XX PT immunity in a patient.

XX PS Example 7; Page 108-111; 118pp; English.

XX XX The present invention is related to the isolation of antigenic sequences

CC from the rodent parasite Babesia microti. This organism is transmitted to

CC humans by the same tick which transmits Lyme disease and ehrlichiosis.

CC The organism causes a malaria-like infection known as babesiosis. The

CC sequences identified by this invention can be used in the diagnosis,

CC prevention and treatment of babesiosis.

XX SQ Sequence 666 AA;

XX DR 16-SEP-1999 (first entry)

XX DE Babesia microti antigen BMNI-17 degenerate repeat sequence.

XX ID AAY24359 standard; peptide; 32 AA.

XX AC AAY24359;

XX XX 16-SEP-1999

XX XX AAY24359

XX KW Babesia microti; antigen; immunogen; diagnosis; infection; vaccine;

XX KW immunity; detection.

XX OS Babesia microti.

XX XX Babesia microti.

XX FH Key Location/Qualifiers

CC The present invention is related to the isolation of antigenic sequences
 CC from the rodent parasite Babesia microti. This organism is transmitted to
 CC humans by the same tick which transmits Lyme disease and ehrlichiosis.
 CC The organism causes a malaria-like infection known as babesiosis. The
 CC sequences identified by this invention can be used in the diagnosis,
 CC prevention and treatment of babesiosis.

XX Sequence 666 AA;

Query Match 100.0%; Score 139; DB 21; Length 666;
 Best Local Similarity 100.0%; Pred. No. 9.4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX

Qy 1 GKPNTNKEKERAERKSHTDTQEQICE 26

Db 403 GKPNTNKEKERAERKSHTDTQEQICE 428

FT	Misc-difference 3	/label= Gly, Asp	AC AAB30208;
FT	Misc-difference 5	/label= Pro, Ile	XX DT 12-FEB-2001 (first entry)
FT	Misc-difference 70	/label= Lys, Thr	XX DE B. microti BMNI-17 antigen reverse complement repeat SEQ ID NO: 39.
FT	Misc-difference 11	/label= Glu, Gly	XX KW Babesiosis; rodent parasite; tick-borne illness; antigen; disease diagnosis; disease prevention.
FT	Misc-difference 12	/label= Lys, Asn	XX KW
FT	Misc-difference 14	/label= Glu, Gly	OS Babesia microti.
FT	Misc-difference 15	/label= Ile, Arg	PN WO20060090-A1.
FT	Misc-difference 18	/label= His, Tyr	PR
FT	Misc-difference 23	/label= Thr, Pro	PD 12-OCT-2000.
FT	Misc-difference 26	/label= Ile, Thr	XX
FT	Misc-difference 27	/label= Cys, Ser	XX PP 05-APR-2000; US09136.
FT	Misc-difference 28	/label= Asp, Glu	XX PR 05-APR-1999; 99US-0286488.
FT	Misc-difference 29	/label= Glu, Ala	PR 17-MAR-2000; 2000US-0528784.
FT	Misc-difference 30	/label= Cys, His	XX PA (CORT-) CORIXA CORP.
FT	W09929869-A1.		XX PI Reed SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD;
XX			XX DR WPI; 2000-686939/67.
XX			XX New polypeptides containing an antigenic portion of Babesia microti antigen and DNA encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient.
XX			XX Claim 6; Page 88; 118pp; English.
XX			XX The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
XX			XX PS Sequence 32 AA;
XX			XX Query Match Score 63; DB 21; Length 32;
XX			XX Best Local Similarity 63.6%; Pred. No. 0.013;
XX			XX Matches 14; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
XX			QY 2 KPNTNIKSEKAERKSHDTQTQEQ 23
PS	Example 1; Page 94; 126pp; English.		ID AAG75092 standard; Protein; 600 AA.
XX			Db 4 KXXNXXNSXXXKSXXSDTQTQEQ 25
CC	The present invention describes isolated polypeptides comprising specific immunogenic portions of Babesia microti. AAX8983 to AAX88994 encode specifically claimed B. microti immunogenic proteins, and AAY24327 to AAX24338 represent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B. microti infections. The present sequence represents a B. microti antigen BMNI-17 degenerate repeat sequence.		RESULT 11 AAG75092
CC			XX DT 03-SEP-2001 (first entry)
CC			XX DE Human colon cancer antigen protein SEQ ID NO:5856.
CC			XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection; colorctal carcinoma; chromosome 21.
CC			OS Homo sapiens.
CC			PN WO200122920-A2.
CC			XX PD 05-APR-2001.
XX	Sequence 32 AA;		XX
XX			XX Query Match Score 63; DB 20; Length 32;
XX			XX Best Local Similarity 63.6%; Pred. No. 0.013;
XX			XX Matches 14; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY	2 KPNTNIKSEKAERKSHDTQTQEQ 23		XX
Db	4 KXXNXXNSXXXKSXXSDTQTQEQ 25		DE
RESULT 10			XX Human colon cancer antigen protein SEQ ID NO:5856.
AAB30208			XX KW
ID AAB30208 standard; Peptide; 32 AA.			OS Homo sapiens.
XX			PN WO200122920-A2.
XX			XX PD 05-APR-2001.
XX			XX PF 28-SEP-2000; 2000WO-US26524.
XX			XX PR 29-SEP-1999; 99US-0157137.

PR 03-NOV-1999; 99US-0163280.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Barash SC, Birse CE, Rosen CA;
 PI WPI; 2001-235357/24.
 DR N-PSDB; AAH34491.
 XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
 XX Claim 11; Page 7370-7373; 9803PP; English.
 PS AAH32943 TO AAH37195 and AAH73514 to AAH77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytotoxic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AB77789 represent sequences used in the exemplification of the present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX SQ Sequence 600 AA;
 Query Match Score 38.8%; DB 22; Length 600;
 Best Local Similarity 46.28%; Pred. No. 9;
 Matches 12; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
 AC AAY68823;
 DE Amino acid sequence of a son of sevenless (Sos) related protein.
 KW Ras; Son of sevenless; Sos; crystal; Ras-Sos complex; cancer;
 KW protein coordinate data.
 XX OS Saccharomyces cerevisiae.
 XX PN WO200005258-A1.
 PD 03-FEB-2000 (first entry)
 XX PR 20-JUL-1999; 99WO-US16348.
 XX PR 21-JUL-1998; 98US-0119794.
 PA (UYRQ) UNIV ROCKEFELLER.
 XX PI Boriack-Sjodin A, Margaret SM, Bar-Sagi D, Cole P, Kuriyan J;
 XX WPI; 2000-182647/16.

XX Novel crystals comprising a Ras-Son of sevenless complex, useful for screening drugs useful in cancer treatment.
 PT PT
 XX XX Disclosure; Page 181-185; 224PP; English.
 PS
 XX The specification describes a crystal complex comprising at least a son of sevenless (Sos) protein catalytic region fragment, that effectively diffracts X-rays. Ras and Sos form a tight complex. Sos does not impede the binding sites for the nucleotide base and the ribose of GTP or GDP and thus the Ras-Sos complex maintains a structure that permits nucleotide release and rebinding. The crystals are used for the determination of the atomic coordinates of the complex to a resolution of more than 5.0 Ångström. The crystals, or a dataset comprising the three dimensional coordinates obtained from the crystals, is useful for identifying an agent that stabilizes the Ras-Sos complex. The crystals are also useful for identifying agents that inhibit the formation of Ras-Sos complex. Ras and Sos fragments are useful for growing a crystal of a protein-ligand complex. Agents that stabilize or inhibit the formation of Ras-Sos complex are useful in the treatment of cancer. The present sequence represents a yeast Sos-related protein.
 XX Sequence 1048 AA;
 Query Match Score 38.8%; DB 21; Length 1048;
 Best Local Similarity 45.0%; Pred. No. 17;
 Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 AC AAY35210;
 DE 11-1 : 11-1 : 11-1 :
 DB 1002 PNSNSNKSQKSRSQDQTE 1021

RESULT 13
 AAY35210
 ID AAY35210 standard; Protein; 212 AA.
 XX
 AC AAY35210;
 DE 13-SEP-1999 (first entry)
 DB Chlamydia pneumoniae protein not found in C. trachomatis.
 XX
 KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
 KW vaccine; neutralising epitope.
 XX
 OS Chlamydia pneumoniae.
 XX PN WO9927105-A2.
 PD 03-JUN-1999.
 XX PF 20-NOV-1998;
 XX PR 04-NOV-1998; 98WO-1B01890.
 PR 21-NOV-1997; 97FR-0014673.
 XX PA (GEST) GENSET.
 XX PI Griffais R;
 XX DR 1999-357842/30.
 XX PT Genome sequence of Chlamydia pneumoniae
 XX PS Page 1060; Disclosure; 1912PP; English.
 XX AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and C. pneumoniae

CC bronchitis and is thought to be a contributing factor in heart
 CC disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in
 CC immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotides sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 epitope of C. pneumoniae.

XX Sequence 212 AA;

Query Match 36.7%; Score 51; DB 20; Length 212;
 Best Local Similarity 38.1%; Pred. No. 8;
 Matches 8; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 6 NKSEERAERKSHDQTQEQICE 26
 Db 19 NQSQRDIQRHDREASQRACE 39

XX

PD 03-JUN-1999.

XX

PF 20-Nov-1998;

XX

PR 04-Nov-1998;

XX

PA 98US-0107078;

XX

PA 21-Nov-1997;

XX

PA 97FR-0014673.

XX

PA (GEST) GENSET.

XX

PI Griffais R;

XX

WPI; 1999-357842/30.

XX

PT Genome sequence of Chlamydia pneumoniae

XX

PS Page 860-861; Disclosure: 1912pp; English.

XX

CC AAY34584-Y35879 represent the proteins encoded by all the open reading

CC frames in the complete genome (see AAX91990) of Chlamydia pneumoniae.

CC C. pneumoniae causes respiratory disease such as pneumonia and

CC bronchitis and is thought to be a contributing factor in heart

CC disease, sarcoidosis, sinusitis, purulent otitis media, erythema

CC nodosum or pharyngitis. The polypeptides encoded by the open reading

CC frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in

CC immunogenic compositions as vaccines. Vectors containing C. pneumoniae

CC nucleotides sequences can also be used as immunogenic compositions,

CC especially where the vector directs the expression of a neutralising

CC epitope of C. pneumoniae.

XX Sequence 584 AA;

Query Match 36.0%; Score 50; DB 20; Length 584;
 Best Local Similarity 30.8%; Pred. No. 36;
 Matches 8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

CC bronchitis and is thought to be a contributing factor in heart
 CC disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in
 CC immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotides sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae.

XX Sequence 584 AA;

Query Match 36.7%; Score 51; DB 20; Length 212;
 Best Local Similarity 38.1%; Pred. No. 8;
 Matches 8; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GKPNTNKSEKAERKSHDQTQEQICE 26
 Db 292 GIPNSNITLERAEKENFKQESREOLSE 317

RESULT 15

AY56656 standard; Protein; 523 AA.

ID AY56656

XX AC AY56656;

XX DT 10-APR-2000 (first entry)

XX DE Morbillivirus antigenic protein.

XX KW Antigenic; nucleocapsid protein; canine distemper virus; CDV;

XX KW Morbillivirus; Paramyxovirus.

OS Morbillivirus sp.

XX PN JP11346768-A.

XX PD 21-DEC-1999.

XX PF 03-JUN-1998;

XX PR 98JP-0155072.

XX PA (MORG) MORINAGA MILK IND CO LTD.

XX WPL: 2000-109685/10.

DR DR N PSDB; AAV46837.

XX PR A protein having antigenicity of canine distemper virus nucleocapsid

XX PT Protein - useful in the diagnosis of canine distemper virus infection

XX PS Disclosure; Page 11-13; 15pp; Japanese.

XX PT The invention provides a protein which has a molecular weight of 58 kD

CC CC and has antigenicity of nucleocapsid protein (NP) of canine distemper

CC CC virus (CDV) belonging to Morbillivirus family.

CC CC The protein can be used to prepare a reagent for the determination of

CC CC anti-CDV NP antibody by immobilizing the above protein on a carrier or a

CC CC membrane as the active component. The reagent can be used for diagnosis

CC CC of CDV infection. Judgement of effect of vaccine and judgement of

CC CC inoculation period. The reagent can determine anti-CDV NP antibody

CC CC contained in canine serum easily. The present sequence represents

CC CC the Morbillivirus antigenic protein.

XX SQ Sequence 523 AA;

Query Match 35.6%; Score 49.5; DB 21; Length 523;

Best Local Similarity 47.6%; Pred. No. 38;

Matches 10; Conservative 5; Mismatches 5;

Indels 1; Gaps 1;

Qy 3 PNTNKSEKAERKSHDQTQEQICE 23

Db 461 PDVNSSERSEPR-HDDQIQQD 480

Search completed: October 11, 2002, 20:37:37

Job time : 64 secs

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Sat, Oct 12 13:34:40 2002

us-09-794-764-195.raii

Page 1

GanCore version 5.1.3							
Copyright (c) 1993 - 2002 Compugen Ltd.							
protein - protein search, using sw model							
run on: October 11, 2002, 20:36:38 ; Search time 33 Seconds (without alignments) 19.244 Million cell updates/sec							
title:	US-09-794-764-195	perfect score:	139	sequence:	1 GKPNTNKEAENKSHDDQTQETICE 26	scoring table:	BLOSUM62
						Gapop 10.0 , Gapext 0.5	
						231628 seqs, 2425554 residues	
total number of hits satisfying chosen parameters:							
						231628	
database :	Issued_Patents_AA,*						
	1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep:*	2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep:*	3: /cgn2_6/ptodata/2/iaa/6A-COMB.pep:*	4: /cgn2_6/ptodata/2/iaa/6B-COMB.pep:*	5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*	6: /cgn2_6/ptodata/2/iaa/Backfiles.pep:*	
post-processing:	Minimum Match 0%	Maximum Match 100%	Listing first 45 summaries				
SUMMARIES							
result No.	Score	Query Length	DB ID	ID	Description		
1	139	100	0	275	4 US-08-845-258-53	Sequence 53, AP	
2	139	100	0	275	4 US-08-930-571-53	Sequence 53, AP	
3	139	100	0	445	4 US-08-845-258-38	Sequence 38, AP	
4	139	100	0	445	4 US-08-990-571-38	Sequence 38, AP	
5	139	100	0	445	4 US-08-723-142A-38	Sequence 38, AP	
6	63	45	3	32	4 US-08-845-258-39	Sequence 39, AP	
7	63	45	3	32	4 US-08-990-571-39	Sequence 39, AP	
8	63	45	3	32	4 US-08-723-142A-39	Sequence 39, AP	
9	54	38	8	1048	3 US-09-356-952-5	Sequence 5, APP	
10	47	33	8	220	2 US-08-841-349-7	Sequence 7, APP	
11	47	33	8	2154	2 US-08-841-349-4	Sequence 4, APP	
12	46	33	1	259	4 US-09-185-160-9	Sequence 9, APP	
13	46	33	1	734	4 US-09-185-160-13	Sequence 13, APP	
14	44	31	7	343	1 US-08-348-792-10	Sequence 10, APP	
15	44	31	7	343	2 US-08-462-738-10	Sequence 17, APP	
16	43	30	9	123	1 US-08-131-625B-17	Sequence 19, APP	
17	43	30	9	123	5 PCT-US95-10904-19	Sequence 8, APP	
18	43	30	9	534	2 US-08-693-814B-8	Sequence 11, APP	
19	43	30	9	731	4 US-09-185-160-11	Sequence 2, APP	
20	43	30	9	752	1 US-08-244-189-2	Sequence 26, APP	
21	42	30	2	461	2 US-08-453-58A-26	Sequence 4, APP	
22	42	30	2	461	2 US-08-463-667A-4	Sequence 26, APP	
23	42	30	2	461	3 US-08-923-634B-26	Sequence 27, APP	
24	42	30	2	461	5 PCT-US91-09133-27	Sequence 2, APP	
25	42	30	2	546	4 US-09-352-990-2	Sequence 12, APP	
26	42	30	2	588	2 US-08-889-419-12	Sequence 12, APP	
27	42	30	2	588	3 US-08-889-419-12	Sequence 12, APP	

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28 42 30 .2 588 5 PCT-US93-07189-12 Sequence 12, Appli
29 42 30 .2 1566 2 US-08-687-556A-23 Sequence 23, Appli
30 42 30 .2 1848 4 US-08-596-791-6 Sequence 6, Appli
31 42 30 .2 1848 5 PCT-US95-10661A-6 Sequence 6, Appli
32 41 .5 29 .9 123 2 US-08-799-164A-13 Sequence 13, Appli
33 41 .5 29 .9 123 4 US-08-686-968C-11 Sequence 11, Appli
34 41 .5 29 .9 123 5 PCT-US95-09927-13 Sequence 13, Appli
35 41 .5 29 .9 123 5 PCT-US95-10904-53 Sequence 53, Appli
36 41 .5 29 .9 123 5 PCT-US95-10904-55 Sequence 55, Appli
37 41 .5 29 .9 123 5 PCT-US95-10904-57 Sequence 57, Appli
38 41 29 .5 26 1 US-07-942-245-455 Sequence 455, Appli
39 41 29 .5 278 2 US-08-722-626B-2 Sequence 2, Appli
40 41 29 .5 330 2 US-08-712-348-2 Sequence 2, Appli
41 41 29 .5 330 4 US-09-145-191-2 Sequence 2, Appli
42 41 29 .5 333 2 US-08-712-948-1 Sequence 1, Appli
43 41 29 .5 411 2 US-08-741-134-6 Sequence 6, Appli
44 41 29 .5 442 4 US-09-347-833-11 Sequence 11, Appli
45 41 29 .5 458 5 PCT-US96-00994-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-845-258-53
; Sequence 53, Application US/08845258
; Patent No. 6183976
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond
; APPLICANT: Sleath, Paul R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; TITLE OF INVENTION: AND TREATMENT OF B. MICOTI INFECTON
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,258
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.426C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 275 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Babesia microti
; ; ORGANISM: Babesia microti

US-08-845-258-53
; Query Match 100.0% Score 139; DB 4; Length 275;
; Best Local Similarity 100.0%; Pred. No. 1.5e-13;
; Matches 26; Conservative 0; Mismatches 0; Indels 0;
; Gaps 0;

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Oy 1 GKPNTNKEAERKSHDTQTQICE 26
 Db 218 GKPNTNKEAERKSHDTQTQICE 243

RESULT 2
 US-08-990-571-53
 ; Sequence 53, Application US/08990571
 ; Patent No. 6214971

GENERAL INFORMATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. M.
 ; NUMBER OF SEQUENCES: 79
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED AND BERRY
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/990,571
 ; FILING DATE: 24-APR-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Maki, David J.
 ; REGISTRATION NUMBER: 31,392
 ; REFERENCE/DOCKET NUMBER: 210121.426C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 38:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 445 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-08-845-258-38

Query Match 100.0%; Score 139; DB 4; Length 445;
 Best Local Similarity 100.0%; Pred. No. 2.5e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 US-08-990-571-38
 ; Sequence 38, Application US/08990571
 ; Patent No. 6214971

GENERAL INFORMATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B.
 ; NUMBER OF SEQUENCES: 79
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED AND BERRY
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/990,571
 ; FILING DATE: 11-DEC-1997
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Maki, David J.
 ; REGISTRATION NUMBER: 31,392
 ; REFERENCE/DOCKET NUMBER: 210121.426C2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 38:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 445 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-08-990-571-38

Query Match 100.0%; Score 139; DB 4; Length 275;
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKPNTNKEAERKSHDTQTQICE 26
 Db 218 GKPNTNKEAERKSHDTQTQICE 243

RESULT 3
 US-08-845-258-38
 ; Sequence 38, Application US/08845258
 ; Patent No. 6183976

GENERAL INFORMATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lodes, Michael J.
 ; APPLICANT: Houghton, Raymond
 ; APPLICANT: Sleath, Paul R.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
 ; TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTON
 ; NUMBER OF SEQUENCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED AND BERRY
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington

Query Match 100.0%; Score 139; DB 4; Length 445;
 Best Local Similarity 100.0%; Pred. No. 2.5e-13; Indels 0; Gaps 0;
 Matches 26; Conservative 0; Mismatches 0;

Qy 1 GKPNTNKSERAERKSHDTOTQOEICE 26
 Db 182 GKPNTNKSERAERKSHDTOTQOEICE 207

RESULT 5

US-08-723-142A-38
 Sequence 38, Application US/08723142A

; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Houghton, Raymond
 ; APPLICANT: Sleath, Paul R.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
 ; NUMBER OF SEQUENCES: 49
 ; TITLE OF INVENTION: AND TREATMENT OF B. MICRIDI INFECTION
 ; NUMBER OF SEQUENCES: 49
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED AND BERRY
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 APPLICATION NUMBER: US/08/723,142A
 FILING DATE: 01-OCT-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.426
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 445 amino acids
 TYPE: amino acid
 STRANDEDNESS: Linear
 TOPOLOGY: Linear

FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 3
 OTHER INFORMATION: /note= "Residue can be either Glu
 or Asp"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 5
 OTHER INFORMATION: /note= "Residue can be either Pro
 or Ile"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 7
 OTHER INFORMATION: /note= "Residue can be either Lys
 or Thr"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 11
 OTHER INFORMATION: /note= "Residue can be either Glu
 or Gly"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 12
 OTHER INFORMATION: /note= "Residue can be either Ile
 or Arg"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 18
 OTHER INFORMATION: /note= "Residue can be either His
 or Tyr"
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 23

RESULT 6

US-08-845-258-39
 Sequence 39, Application US/08845258

; GENERAL INFORMATION:
 ; Paten. No. 6183976
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Houghton, Raymond
 ; APPLICANT: Sleath, Paul R.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
 ; NUMBER OF SEQUENCES: 49
 ; TITLE OF INVENTION: AND TREATMENT OF B. MICRIDI INFECTION

RE
3
09
5
1

STRANDEDNESS: OTHER INFORMATION: /note= "Residue can be either Thr or Pro" FEATURE: Modified-site LOCATION: 26 OTHER INFORMATION: /note= "Residue can be either Ile or Thr" FEATURE: Modified-site LOCATION: 27 OTHER INFORMATION: /note= "Residue can be either Cys or Ser" FEATURE: Modified-site LOCATION: 28 OTHER INFORMATION: /note= "Residue can be either Asp or Glu" OTHER INFORMATION: /note= "Residue can be either Ala" FEATURE: Modified-site LOCATION: 29 OTHER INFORMATION: /note= "Residue can be either Glu or Ala" OTHER INFORMATION: /note= "Residue can be either Cys or His" OTHER INFORMATION: US-08-845-258-39

Query Match 2 KPTNPKSAERKSHDTQTE 345 3% ; Score 63; DB 4; Length 32; Best Local Similarity 65.6%; Pred. NO. 0.004; Indels 0; Gaps 0; Mismatches 8; Indels 0; Gaps 0; OTHER INFORMATION: /note= "Residue can be either Cys or His"

Query 2 KPTNPKSAERKSHDTQTE 345 3% ; Score 63; DB 4; Length 32; Best Local Similarity 65.6%; Pred. NO. 0.004; Indels 0; Gaps 0; Mismatches 8; Indels 0; Gaps 0; OTHER INFORMATION: /note= "Residue can be either Cys or His"

Query 4 KXDNKSKXXAXXSDIQTQXE 25

RESULT 7 US-08-930-571-39 Sequence 39, Application US/0890571 GENERAL INFORMATION: Patent No. 6214911 APPLICANT: REED, STEVEN G. ET AL. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. M. NUMBER OF SEQUENCES: 79 CORRESPONDENCE ADDRESS: ADDRESSEE: SEED AND BERRY STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle STATE: Washington COUNTRY: USA ZIP: 98104 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/990,571 FILING DATE: 11-DEC-1997 CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: MAKI, DAVID J. REGISTRATION NUMBER: 31,392 REFERENCE/DOCKET NUMBER: 2110121-426C2 TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900 TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS: LENGTH: 32 amino acids TYPE: amino acid

FEATURE: Modified-site LOCATION: 3 OTHER INFORMATION: /note= "Residue can be either Gly or Asp" FEATURE: Modified-site LOCATION: 5 OTHER INFORMATION: /note= "Residue can be either Pro or Ile" FEATURE: Modified-site LOCATION: 7 OTHER INFORMATION: /note= "Residue can be either Lys or Thr" FEATURE: Modified-site LOCATION: 11 OTHER INFORMATION: /note= "Residue can be either Glu or Gly" FEATURE: Modified-site LOCATION: 12 OTHER INFORMATION: /note= "Residue can be either Lys or Arg" FEATURE: Modified-site LOCATION: 14 OTHER INFORMATION: /note= "Residue can be either Glu or Tyr" FEATURE: Modified-site LOCATION: 18 OTHER INFORMATION: /note= "Residue can be either His or Cys" FEATURE: Modified-site LOCATION: 23 OTHER INFORMATION: /note= "Residue can be either Thr or Pro" FEATURE: Modified-site LOCATION: 15 OTHER INFORMATION: /note= "Residue can be either Ile or Arg" FEATURE: Modified-site LOCATION: 26 OTHER INFORMATION: /note= "Residue can be either Cys or Ser" FEATURE: Modified-site LOCATION: 28 OTHER INFORMATION: /note= "Residue can be either Ala" FEATURE: Modified-site LOCATION: 29 OTHER INFORMATION: /note= "Residue can be either Glu or His" OTHER INFORMATION: US-08-990-571-39

Query Match 45.3%; Score 63; DB 4; Length 32;
 Best Local Similarity 63.6%; Pred. No. 0.004;
 Matches 14; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

LOCATION: 12
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 or Asn"
 FEATURE:
 NAME/KEY: Modified-site

LOCATION: 14
 OTHER INFORMATION: /note= "Residue can be either Glu
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 FEATURE:
 NAME/KEY: Modified-site

LOCATION: 15
 OTHER INFORMATION: /note= "Residue can be either Ile
 or Arg"
 FEATURE:
 NAME/KEY: Modified-site

LOCATION: 18
 OTHER INFORMATION: /note= "Residue can be either His
 or Tyr"
 FEATURE:
 NAME/KEY: Modified-site

LOCATION: 23
 OTHER INFORMATION: /note= "Residue can be either Thr
 or Pro"
 FEATURE:
 NAME/KEY: Modified-site

LOCATION: 26
 OTHER INFORMATION: /note= "Residue can be either Ile
 or Thr"
 FEATURE:
 NAME/KEY: Modified-site

LOCATION: 27
 OTHER INFORMATION: /note= "Residue can be either Cys
 or Ser"
 FEATURE:
 NAME/KEY: Modified-site

LOCATION: 28
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 or Glu"
 FEATURE:
 NAME/KEY: Modified-site

LOCATION: 29
 OTHER INFORMATION: /note= "Residue can be either Glu
 or Ala"
 FEATURE:
 NAME/KEY: Modified-site

LOCATION: 30
 OTHER INFORMATION: /note= "Residue can be either Cys
 or His"
 FEATURE:
 NAME/KEY: Modified-site

Query Match 45.3%; Score 63; DB 4; Length 32;
 Best Local Similarity 63.6%; Pred. No. 0.004;
 Matches 14; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

RESULT 9
 US-09-356-952-5
 OTHER INFORMATION: /note= "Residue can be either Lys
 or Ile"
 FEATURE:
 NAME/KEY: Modified-site

LOCATION: 7
 OTHER INFORMATION: /note= "Residue can be either Lys
 or Thr"
 FEATURE:
 NAME/KEY: Modified-site

LOCATION: 11
 OTHER INFORMATION: /note= "Residue can be either Glu
 or Gly"
 FEATURE:
 NAME/KEY: Modified-site

RESULT 5
 Sequence 5, Application US/09356952
 ; Patent No. 6117663
 GENERAL INFORMATION:
 ; APPLICANT: Boriack-Sjodin, Ann
 ; OTHER INFORMATION: Margarit, S. M.
 ; APPLICANT: Bor-Sogi, Dafna
 ; APPLICANT: Cole, Phillip
 ; APPLICANT: Kuriyan, John
 ; TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
 ; FILE REFERENCE: 600-1-228N
 ; CURRENT APPLICATION NUMBER: US/09/356,952

RESULT 12
 CURRENT FILING DATE: 1999-07-19
 ; EARTIER APPLICATION NUMBER: 60/093,631
 ; EARTIER FILING DATE: 1998-07-21
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 1048
 ; TYPE: PRT
 ; ORGANISM: *Saccharomyces cerevisiae*
 US-09-356-952-5

Query Match 38.8%; Score 54; DB 3; Length 1048;
 Best Local Similarity 45.0%; Pred. No. 5.1;
 Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

CY 3 PNTNKEKAKRKSHTQTTQ 22
 Db 1002 PNSNSNKSOKSRDQTDE 1021

RESULT 10
 US-08-841-349-7
 ; Sequence 7, Application US/08841349B
 ; Patent No. 5955594
 ; GENERAL INFORMATION:
 ; APPLICANT: MISHRA, LOPA
 ; TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT. . .
 ; FILE REFERENCE: XX/P04470US0
 ; CURRENT APPLICATION NUMBER: US/08/841,349B
 ; CURRENT FILING DATE: 1997-04-30
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 220
 ; TYPE: PRT
 ; ORGANISM: *Mus musculus*
 US-08-841-349-7

Query Match 33.8%; Score 47; DB 2; Length 220;
 Best Local Similarity 37.5%; Pred. No. 9.8;
 Matches 9; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Cy 3 PNTNKEKAKRKSHTQTTQBE 26
 Db 158 PNTKVSEAESQQWDTSKGDQVSQ 181

RESULT 11
 US-08-841-349-4
 ; Sequence 4, Application US/08841349B
 ; Patent No. 5955594
 ; GENERAL INFORMATION:
 ; APPLICANT: MISHRA, LOPA
 ; TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT. . .
 ; FILE REFERENCE: XX/P04470US0
 ; CURRENT APPLICATION NUMBER: US/08/841,349B
 ; CURRENT FILING DATE: 1997-04-30
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 2154
 ; TYPE: PRT
 ; ORGANISM: *Mus musculus*
 US-08-841-349-4

Query Match 33.8%; Score 47; DB 2; Length 2154;
 Best Local Similarity 37.5%; Pred. No. 1.4e+02;
 Matches 9; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 3 PNTNKEKAKRKSHTQTTQBE 26
 Db 2092 PNTKVSEAESQQWDTSKGDQVSQ 2115

RESULT 13
 US-09-185-160-13
 ; Sequence 13, Application US/09185160
 ; Patent No. 6252137
 ; GENERAL INFORMATION:
 ; APPLICANT: HARDER, PATRICIA A.
 ; TITLE OF INVENTION: SOYBEAN HOMOLOG OF A SEED-SPECIFIC
 ; TRANSCRIPTION ACTIVATOR FROM PHASEOLUS
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: E. I. DUPONT DE Nemours and Company
 ; STREET: 1007 Market Street
 ; CITY: Wilmington
 ; STATE: Delaware
 ; COUNTRY: USA

Query Match 33.1%; Score 46; DB 4; Length 259;
 Best Local Similarity 42.1%; Pred. No. 17;
 Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 2 KPNTNKEKAKRKSHTQ 20
 Db 212 KPETKKAGSKSQKNQHGTG 230

RESULT 13
 US-09-185-160-13
 ; Sequence 13, Application US/09185160
 ; Patent No. 6252137
 ; GENERAL INFORMATION:
 ; APPLICANT: HARDER, PATRICIA A.
 ; TITLE OF INVENTION: SOYBEAN HOMOLOG OF A SEED-SPECIFIC
 ; TRANSCRIPTION ACTIVATOR FROM PHASEOLUS
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: E. I. DUPONT DE Nemours and Company
 ; STREET: 1007 Market Street
 ; CITY: Wilmington
 ; STATE: Delaware
 ; COUNTRY: USA

ZIP: 19898
 COMPUTER READABLE FORM:
 MEDIUM TYPE: DISKETTE, 3.50 INCH
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: MICROSOFT WINDOWS 95
 SOFTWARE: MICROSOFT WORD VERSION 7.0A
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-09/185,160
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/065,459
 FILING DATE: NOVEMBER 12, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: MAJARIAN, WILLIAM R.
 REGISTRATION NUMBER: 41,173
 REFERENCE/DOCKET NUMBER: BB-1096
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 302-773-0162
 TELEX/FAX: 302-992-4926
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 734 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-09-185-160-13

Query Match Score 46; DB 4; Length 734;
 Best Local Similarity 42.1%; Pred. No. 56;
 Matches 8; Conservative 4; Mismatches 7;
 Indels 0; Gaps 0;

Qy 2 KPNTNESEKAERKSHDQT 20
 Db 687 KPETKAGKSQRNQHGTGT 705

RESULT 14 US-08-792-10
 Sequence 10, Application US/08348792
 Patent No. 557643
 GENERAL INFORMATION:
 APPLICANT: Aversa, Gregorio
 APPLICANT: Chang, Chia-Chun J.
 APPLICANT: Cocks, Benjamin G.
 APPLICANT: de Vries, Jan E.
 TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
 NUMBER OF SEQUENCES: 12
 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104

Computer Readable Form:
 Medium Type: Floppy disk
 Computer: IBM PC compatible
 Operating System: PC-DOS/MS-DOS
 Software: Patentin Release #1.0, Version #1.25
 Current Application Data:
 Application Number: US/08/462,738
 Filing Date: 05-JUN-1995
 Classification: 435
 Prior Application Data:
 Application Number: US 08/462,738
 Filing Date: 02-DEC-1994
 Attorney/Agent Information:
 Name: Ching, Edwin P.
 Registration Number: 34,090
 Reference/Docket Number: DX0436GB
 Telecommunication Information:
 Telephone: 415-852-9196
 Telefax: 415-496-1200
 Information for Seq ID No: 10:
 Sequence Characteristics:
 Length: 343 amino acids
 Type: amino acid
 Topology: linear
 Molecule Type: protein
 US-08-462-738-10

Query Match Score 44; DB 2; Length 343;
 Best Local Similarity 47.4%; Pred. No. 47;
 Matches 9; Conservative 2; Mismatches 8;
 Indels 0; Gaps 0;

Qy 7 KSEKAERKSHDQT 25
 Db 293 KSGPQEKKLHDALTQDPC 311

Job time : 34 secs

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